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Run on: November 10, 2004, 18:00:33 ; Search time 156 Seconds	(without alignments)									
Scoring table: BL0SUM62	78.185 Million cell updates/sec									
Searched: GapOp 10.0 , Gapext: 0.5	US-10-685-435-15									
Total number of hits satisfying chosen parameters: 2002273	185 100.0 809 8 ADP71140									
Minimum DB seq length: 0	184 99.5 192 2 AAR69647									
Maximum DB seq length: 200000000	184 99.5 192 2 AAR69652									
Post-processing: Minimum Match 0%	184 99.5 192 2 AAR69656									
Listing first 45 summaries	184 99.5 192 2 AAR69642									
Database : A_Geneseq_23Sep04:*	184 99.5 192 2 AAR69642									
1: geneseqp1980s:*	184 99.5 192 2 AAR69642									
2: geneseqp1990s:*	184 99.5 192 2 AAR69642									
3: geneseqp2000s:*	184 99.5 192 2 AAR69642									
4: geneseqp2001s:*	184 99.5 192 2 AAR69642									
5: geneseqp2002s:*	184 99.5 192 2 AAR69642									
6: geneseqp2003bs:*	184 99.5 192 2 AAR69642									
7: geneseqp2004s:*	184 99.5 192 2 AAR69642									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	184 99.5 192 2 AAR69642									
SUMMARIES	184 99.5 192 2 AAR69642									
RESULT 1	184 99.5 192 2 AAR69642									
ID AAV39498 standard; peptide; 34 AA.	184 99.5 192 2 AAR69642									
XX AAV39498;	184 99.5 192 2 AAR69642									
XX 27-AUG-2003 (revised)	184 99.5 192 2 AAR69642									
XX DT 22-NOV-1999 (first entry)	184 99.5 192 2 AAR69642									
XX DE HCV E1 protein residues 307-340.	184 99.5 192 2 AAR69642									
XX KW HCV; E1 protein; E2 protein; epitope; hepatitis c virus; antibody; detection; HCV protein antigen.	184 99.5 192 2 AAR69642									
XX OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX PN ER947525-A1.	184 99.5 192 2 AAR69642									
XX PD 06-OCT-1999.	184 99.5 192 2 AAR69642									
XX PF 27-MAR-1998; 98EP-00870060.	184 99.5 192 2 AAR69642									
XX PR 27-MAR-1998; 98EP-00870060..	184 99.5 192 2 AAR69642									
XX PA (INNO-) INNOCGENETICS NV.	184 99.5 192 2 AAR69642									
XX DR WPI; 1999-542955/46.	184 99.5 192 2 AAR69642									
XX PT New anti-Hepatitis C virus (HCV) antibodies useful for in situ detection of HCV.	184 99.5 192 2 AAR69642									
XX Example 4; Page 9; 32pp; English.	184 99.5 192 2 AAR69642									
XX This sequence represents residues 307-340 of the hepatitis c virus (HCV) E1 protein. The invention relates to an antibody (Ab) or its derivative that specifically binds to the C-terminal region of the HCV E1 protein (amino acids (aa) 327-383) or the N-terminal region of the HCV E2 protein (aa 384-450). The Ab allows the in situ detection of HCV protein antigens. The Ab is used to detect the HCV E1 or E2 proteins in human peripheral blood cells or liver tissue. It may also be used to detect HCV in other tissue and fluid samples such as serum, plasma, saliva, mucus and sections or biopsies such as from skin. (Updated on 27-AUG-2003 to correct OS field.)	184 99.5 192 2 AAR69642									
XX Sequence 34 AA;	184 99.5 192 2 AAR69642									
Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 192 2 AAR69642									
XX Query Match 100.0%; Score 185; DB 2; Length 34;	184 99.5 192 2 AAR69642									
Best Local Similarity 100.0%; Pred. No. 9e-21;	184 99.5 192 2 AAR69642									
OS Hepatitis C virus.	184 99.5 19									

CC envelope protein (selected from an E1 protein and/or an E2 protein, and their parts, and optionally, a pharmaceutical adjuvant) and an HCV vaccine composition (comprising a recombinant envelope protein chosen from an E1 protein and/or an E2 protein, and parts of the E1 and E2 Proteins and, optionally, a pharmaceutical adjuvant. The HCV vaccine composition is useful for reducing liver disease (such as liver fibrosis or its progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in the liver in a chronic HCV-infected mammal, or for treating a chronic HCV -infected mammal, particularly human. The HCV E1 proteins are useful for in vitro monitoring HCV disease or prognosis the response to treatment of patients suffering from HCV infection. The present sequence is an HCV E1 protein lacking its hydrophobic domain.

XX SQ Sequence 200 AA;

Query Match 100.0%; Score 185; DB 8; Length 200;
Best Local Similarity 100.0%; Pred. No. 7.7e-20; Mismatches 0; Indels 0; Gaps 0;

CC Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGERMAWMNMNSPTTALVSQLRI 34
Db 166 SIYPGHITGHRWAWDMNMNSPTTALVSQLRI 199

XX RESULT 10

XX ADD5536
ID ADD5536 standard; protein; 210 AA.

XX AC ADD5536;
XX DT 15-JAN-2004 (first entry)

XX DE Hepatitis C virus E1/E2 protein #4.
XX Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;

XX KW liver fibrosis.
XX OS Hepatitis C virus.

XX PN WO2003051912-A2.

XX PC 26-JUN-2003.

XX PF 18-DEC-2002; 2002WO-EP01440.

XX PR 18-DEC-2001; 2001US-00020510.

XX PR 16-OCT-2002; 2002US-0418358P.

XX PA (INNO-) INNOCENTICS NV.

XX PI Maertens G, Depla E, Bosman F;

XX DR WIT; 2003-541632/51.

XX DR N-PSDB; ADD5535.

XX PT New hepatitis C virus (HCV) vaccine composition, useful for reducing liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.

XX PS Disclosure; SEQ ID NO 28; 271PP; English.

CC The invention comprises an Hepatitis C virus (HCV) vaccine for reducing liver disease. The vaccine of the invention comprises an HCV E1 or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present amino acid sequence represents an HCV E1/E2 protein.

XX SQ Sequence 210 AA;

Query Match 100.0%; Score 185; DB 7; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.7e-20; Mismatches 0; Indels 0; Gaps 0;

CC Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRWAWDMNMNSPTTALVSQLRI 34
Db 166 SIYPGHITGHRWAWDMNMNSPTTALVSQLRI 199

CC treatment of patients suffering from HCV infection. The present sequence is a protein described in the exemplification of the invention

XX SQ Sequence 210 AA;

Query Match 100.0%; Score 185; DB 5; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.7e-20; Mismatches 0; Indels 0; Gaps 0;

CC Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRWAWDMNMNSPTTALVSQLRI 34
Db 166 SIYPGHITGHRWAWDMNMNSPTTALVSQLRI 199

CC The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV) single or specific oligomeric composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosis the response to

DT 23-SEP-2004 (first entry)
 XX DE
 XX HCV E1 protein hydrophobic region I deletion mutant HC1140.
 XX Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
 KW liver disease; liver fibrosis; mutant; steatosis;
 KW serum alanine aminotransferase level; steatosis;
 KW anti-E2 immunoreactivity; vaccine; mutant.
 XX OS Hepatitis C virus.
 OS Synthetic.
 XX PN US2004126395-A1.
 XX PD 01-JUL-2004.
 XX PP 18-DEC-2002; 2002US-00321798.
 XX PR 18-DEC-2001; 2001US-0453708P.
 PR 16-OCT-2002; 2002US-0418358P.
 XX PA (MAER/)
 PA (DEPL/)
 PA (BOSM/)
 PT Maertens G, Depla E, Bosman F;
 PT XX
 DR N-PSDB; ADB7117.
 XX
 PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver
 PT disease, serum alanine aminotransferase levels, steatosis, or anti-E2
 PT immunoreactivity in the liver of a chronic HCV-infected mammal.
 XX
 XX Example 2; SEQ ID NO 28; 176pp; English.
 PS
 CC The invention relates to the use of a hepatitis C virus (HCV) vaccine
 CC composition for reducing liver disease (such as liver fibrosis or its
 CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or
 CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
 CC or for treating a chronic HCV-infected mammal. The liver disease is
 CC reduced by at least 1-2 points according to the overall Ishak score in
 CC the HCV-infected mammal. Also included are a method for predicting
 CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic
 CC combination of at least 2 HCV single or specific oligomeric recombinant
 CC envelope protein selected from an E1 or E2 protein, a part of E1 and E2
 CC proteins, an E1/E2 protein complex formed from purified HCV single or
 CC specific oligomeric recombinant E1 or E2 proteins or its parts and
 CC optionally a pharmaceutical adjuvant), a composition (comprising at least
 one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an
 CC immunogenic HCV composition (or HCV vaccine composition) comprising a
 CC recombinant virus allowing expression of at least one HCV recombinant
 CC envelope protein (selected from an E1 protein and/or an E2 protein, and
 CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV
 CC vaccine composition (comprising a recombinant virus allowing expression
 CC of at least one HCV recombinant envelope protein chosen from an E1
 CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
 CC optionally, a pharmaceutical adjuvant. The HCV vaccine composition is
 CC useful for reducing liver disease (such as liver fibrosis or its
 CC progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
 CC the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
 CC -infected mammal, particularly human. The HCV E1 proteins are useful for
 CC in vitro monitoring HCV disease or prognosis the response to treatment
 CC of patients suffering from HCV infection. The present sequence is an HCV
 CC E1 protein lacking its hydrophobic domain.
 XX Sequence 210 AA;

Query Match 100.0%; Score 185; DB 8; Length 210;
 Best Local Similarity 100.0%; Pred. No. 7; 7e-20;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ Sequence 210 AA:
 RESULT 13
 ADD5512 ID ADD5512 standard; protein; 212 AA.
 XX AC ADD5512;
 XX

DT 15-JAN-2004 (first entry)
 XX
 DE Hepatitis C virus E1 protein #1.
 XX
 KW Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
 liver fibrosis.
 XX
 OS Hepatitis C virus.
 XX
 PN WO2003051912-A2.
 XX
 PD 26-JUN-2003.
 XX
 PR 18-DEC-2002; 2002WO-EP014480.
 XX
 PR 18-DEC-2001; 2001US-00020510.
 XX
 PR 16-OCT-2002; 2002US-0418358P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Maertens G, Depla E, Bosman F;
 XX
 DR WO2003051912-A2.
 XX
 PR 18-DEC-2001; 2001US-00020510.
 XX
 PR 16-OCT-2002; 2002US-0418358P.
 XX
 PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver
 disease, serum alanine aminotransferase levels, steatosis, or anti-E2
 immunoreactivity in the liver of a chronic HCV-infected mammal.
 XX
 PS Example 2; SEQ ID NO 4; 176pp; English.
 XX
 CC The invention relates to the use of a hepatitis C virus (HCV) vaccine
 composition for reducing liver disease (such as liver fibrosis or its
 progression), serum alanine aminotransferase (ALT) levels, steatosis, or
 anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
 or for treating a chronic HCV-infected mammal. The liver disease is
 reduced by at least 1-2 points according to the overall Ishak score in
 the HCV-infected mammal. Also included are a method for predicting
 changes in liver disease in a chronic HCV-infected mammal, a therapeutic
 HCV vaccine composition (comprising at least one purified or a
 combination of at least 2 HCV single or specific oligomeric recombinant
 envelope protein selected from an E1 or E2 protein, a part of E1 and E2
 proteins, an E1/E2 protein complex formed from purified HCV single or
 specific oligomeric recombinant E1 or E2 proteins or its parts and
 optionally a pharmaceutical adjuvant), a composition (comprising at least
 one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant) an
 immunogenic HCV composition (or HCV vaccine composition) comprising a
 recombinant virus allowing expression of at least one HCV recombinant
 envelope protein (selected from an E1 protein and/or an E2 protein, and
 their parts, and optionally, a pharmaceutical adjuvant) and an HCV
 vaccine composition comprising a recombinant virus allowing expression
 of at least one HCV recombinant envelope protein chosen from an E1
 protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
 optionally, a pharmaceutical adjuvant. The HCV vaccine composition is
 useful for reducing liver disease (such as liver fibrosis or its
 progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
 the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
 -infected mammal, particularly human. The HCV E1 proteins are useful for
 in vitro monitoring HCV disease or prognosing the response to treatment
 of patients suffering from HCV infection. The present sequence is an HCV
 E1 protein (or fragment).
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 185; DB 7; Length 212;
 Best Local Similarity 100.0%; Pred. No. 7.7e-20; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qr 1 SIYPGHITGHRMADMNNNSPTALTVALVSQLRI 34
 Db 139 SIYPGHITGHRMADMNNNSPTALTVALVSQLRI 172

RESULT 14

ADP71094
 ID ADP71094 standard; protein; 212 AA.
 XX
 AC ADP71094;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE HCV E1 protein HCC19A.
 XX
 KW Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
 liver disease; liver fibrosis; immunogen; serum alanine aminotransferase level; steatosis;
 anti-E2 immunoreactivity; vaccine.
 OS Hepatitis C virus.

XX
 PN US2004126195-A1.
 XX
 PD 01-JUL-2004.
 XX
 PR 18-DEC-2002; 2002US-00321798.
 XX
 PR 18-DEC-2001; 2001US-0453708P.
 XX
 PR 16-OCT-2002; 2002US-0418358P.

PA (MAER/); MAERTENS G.
 PA (DEPL/); DEPLA E.
 PA (BOSM/); BOSMAN F.
 XX
 PI Maertens G, Depla E, Bosman F;
 XX
 DR WO2004-99089/47.
 XX
 PR N-PSDB; ADP71093.
 XX
 PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver
 disease, serum alanine aminotransferase levels, steatosis, or anti-E2
 immunoreactivity in the liver of a chronic HCV-infected mammal.
 XX
 PS Example 2; SEQ ID NO 4; 176pp; English.
 XX
 CC The invention relates to the use of a hepatitis C virus (HCV) vaccine
 composition for reducing liver disease (such as liver fibrosis or its
 progression), serum alanine aminotransferase (ALT) levels, steatosis, or
 anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
 or for treating a chronic HCV-infected mammal. The liver disease is
 reduced by at least 1-2 points according to the overall Ishak score in
 the HCV-infected mammal. Also included are a method for predicting
 changes in liver disease in a chronic HCV-infected mammal, a therapeutic
 HCV vaccine composition (comprising at least one purified or a
 combination of at least 2 HCV single or specific oligomeric recombinant
 envelope protein selected from an E1 or E2 protein, a part of E1 and E2
 proteins, an E1/E2 protein complex formed from purified HCV single or
 specific oligomeric recombinant E1 or E2 proteins or its parts and
 optionally a pharmaceutical adjuvant), a composition (comprising at least
 one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant) an
 immunogenic HCV composition (or HCV vaccine composition) comprising a
 recombinant virus allowing expression of at least one HCV recombinant
 envelope protein (selected from an E1 protein and/or an E2 protein, and
 their parts, and optionally, a pharmaceutical adjuvant) and an HCV
 vaccine composition comprising a recombinant virus allowing expression
 of at least one HCV recombinant envelope protein chosen from an E1
 protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
 optionally, a pharmaceutical adjuvant. The HCV vaccine composition is
 useful for reducing liver disease (such as liver fibrosis or its
 progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
 the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
 -infected mammal, particularly human. The HCV E1 proteins are useful for
 in vitro monitoring HCV disease or prognosing the response to treatment
 of patients suffering from HCV infection. The present sequence is an HCV
 E1 protein (or fragment).
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 185; DB 8; Length 212;
 Best Local Similarity 100.0%; Pred. No. 7.7e-20; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qr 1 SIYPGHITGHRMADMNNNSPTALTVALVSQLRI 34
 Db 139 SIYPGHITGHRMADMNNNSPTALTVALVSQLRI 172

RESULT 15

AC018666
 ID AC018666 standard; protein; 239 AA.
 XX
 AC AC018666;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Hepatitis C virus clone HCC137 E1 protein.
 XX
 KW Hepatitis C virus; HCV; E1 protein; E2 protein; infection; virucide;
 immunostimulant; vaccine.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200255548-A2.

PD 18-JUL-2002.
 XX
 XX
 PF 11-JAN-2002; 2002WO-EP000219.
 XX
 PR XX
 PT 11-JAN-2001; 2001US-026669P.
 XX
 PR 30-AUG-2001; 2001US-031576P.
 XX
 PA XX
 (INNO-) INNOGENETICS NV.
 XX
 PI Maertens G, Bosman F, Buyse M;
 DR XX
 DR WPI; 2002-539657/64.
 XX
 DR N-PSDB; AAL48925.
 XX
 PT New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein E1 or E2, useful for immunizing humans from HCV infection.
 XX
 PS Disclosure; Page 174-175; 243PP; English.
 XX
 CC The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prophanising the response to treatment of patients suffering from HCV infection. The present sequence is a protein described in the exemplification of the invention
 XX
 SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 5; Length 239;
 Best Local Similarity 100.0%; Pred. No. 8 9e-20; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 SIVPGHITGHRAWMDDMMNNNSPTALVVSQQLRI 34
 Db 166 SIVPGHITGHRAWMDDMMNNNSPTALVVSQQLRI 199

RESULT 17
 ADP7112 standard; Protein: 239 AA.
 ID ADP7112;
 XX
 AC ADP7112;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE HCV E1 protein hydrophobic region I deletion mutant HCC137.
 XX
 KW Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
 KW liver disease; liver fibrosis; muttein;
 KW serum alanine aminotransferase; level; statosis;
 XX
 OS Synthetic.
 XX
 PN US2004126395-A1.
 XX
 PD 01-JUL-2004.
 XX
 PF 18-DEC-2002; 2002US-00321798.
 XX
 PR 18-DEC-2001; 2001US-0453708P.
 PR 16-OCT-2002; 2002US-0418358P.
 XX
 PA (MAER/) MAERTENS G.
 PA (DBPL/) DEPLA E.
 PA (BOSM/) BOSMAN F.
 XX
 PI Maertens G, Depla E, Bosman F;
 XX
 DR WPI; 2004-499089/47.
 XX
 DR N-PSDB; ADP7111.
 XX
 PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver disease; serum alanine aminotransferase levels; statosis, or anti-E2 immunoactivity in the liver of a chronic HCV-infected mammal.
 XX
 PS Example 2; SEQ ID NO 22; 176PP; English.
 XX
 CC The invention relates to the use of a hepatitis C virus (HCV) vaccine composition for reducing liver disease (such as liver fibrosis or its progression), serum alanine aminotransferase (ALT) levels, statosis, or anti-E2 immunoactivity in the liver of a chronic HCV-infected mammal. The liver disease is present amino acid sequence represents an HCV E1/E2 protein.
 XX
 SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 7; Length 239;
 Best Local Similarity 100.0%; Pred. No. 8 9e-20; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 SIVPGHITGHRAWMDDMMNNNSPTALVVSQQLRI 34
 Db 166 SIVPGHITGHRAWMDDMMNNNSPTALVVSQQLRI 199

RESULT 17
 ADP7112 standard; Protein: 239 AA.
 ID ADP7112;
 XX
 AC ADP7112;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE HCV E1 protein hydrophobic region I deletion mutant HCC137.
 XX
 KW Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
 KW liver disease; liver fibrosis; muttein;
 KW serum alanine aminotransferase; level; statosis;
 XX
 OS Synthetic.
 XX
 PN US2004126395-A1.
 XX
 PD 01-JUL-2004.
 XX
 PF 18-DEC-2002; 2002US-00321798.
 XX
 PR 18-DEC-2001; 2001US-0453708P.
 PR 16-OCT-2002; 2002US-0418358P.
 XX
 PA (MAER/) MAERTENS G.
 PA (DBPL/) DEPLA E.
 PA (BOSM/) BOSMAN F.
 XX
 PI Maertens G, Depla E, Bosman F;
 XX
 DR WPI; 2004-499089/47.
 XX
 DR N-PSDB; ADP7111.
 XX
 PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver disease; serum alanine aminotransferase levels; statosis, or anti-E2 immunoactivity in the liver of a chronic HCV-infected mammal.
 XX
 PS Example 2; SEQ ID NO 22; 176PP; English.
 XX
 CC The invention relates to the use of a hepatitis C virus (HCV) vaccine composition for reducing liver disease (such as liver fibrosis or its progression), serum alanine aminotransferase (ALT) levels, statosis, or anti-E2 immunoactivity in the liver of a chronic HCV-infected mammal. The liver disease is

CC

reduced by at least 1-2 points according to the overall Ishak score in the HCV-infected mammal. Also included are a method for predicting changes in liver disease; in a chronic HCV-infected mammal, a therapeutic HCV vaccine composition (comprising at least one purified or a combination of at least 2 HCV single or specific oligomeric recombinant envelope protein selected from an E1 or E2 protein, a part of E1 and E2 proteins, an E1/E2 protein complex formed from purified HCV single or specific oligomeric recombinant E1 or E2 proteins or its parts and optionally a pharmaceutical adjuvant), a composition comprising at least one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an immunogenic HCV composition (or HCV vaccine composition) comprising a recombinant virus allowing expression of at least one HCV recombinant envelope protein (selected from an E1 protein and/or an E2 protein, and their parts, and optionally, a pharmaceutical adjuvant) and an HCV vaccine composition (comprising a recombinant virus allowing expression of at least one HCV recombinant envelope protein chosen from an E1 protein and/or an E2 protein, and, optionally, a pharmaceutical adjuvant. The HCV vaccine composition is useful for reducing liver disease (such as liver fibrosis or its progression), serum ALT levels, steatosis, and/or anti-E2 immunoreactivity in the liver in a chronic HCV-infected mammal, or for treating a chronic HCV-infected mammal, particularly human. The HCV E1 proteins are useful for in vitro monitoring HCV disease or prognosis the response to treatment of patients suffering from HCV infection. The present sequence is an HCV E1 protein lacking its hydrophobic domain.

SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.98-20; Mismatches 34; Conservative 0; Indels 0; Gaps 0;
Oy 1 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 199

SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.98-20; Mismatches 34; Conservative 0; Indels 0; Gaps 0;
Oy 1 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 199

SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.98-20; Mismatches 34; Conservative 0; Indels 0; Gaps 0;
Oy 1 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 199

SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.98-20; Mismatches 34; Conservative 0; Indels 0; Gaps 0;
Oy 1 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 199

SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.98-20; Mismatches 34; Conservative 0; Indels 0; Gaps 0;
Oy 1 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 199

SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.98-20; Mismatches 34; Conservative 0; Indels 0; Gaps 0;
Oy 1 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 199

SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.98-20; Mismatches 34; Conservative 0; Indels 0; Gaps 0;
Oy 1 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 199

PS Disclosure; Page 162-163; 243pp; English.

The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosis the response to treatment of patients suffering from HCV infection. The present sequence is a protein described in the exemplification of the invention

SQ Sequence 263 AA;

Query Match 100.0%; Score 185; DB 5; Length 263;
Best Local Similarity 100.0%; Pred. No. 1e-19; Mismatches 34; Conservative 0; Indels 0; Gaps 0;
Oy 1 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 34
Do 190 SIYPGHTGHRMADMNNWSPTTALVVSQRLI 223

RESULT 19

ADD5514

ADD5514 standard; protein; 263 AA.

XX

ADD5514;

XX

15-JAN-2004 (first entry)

DE

Hepatitis C virus E1 protein #2.

XX

Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein; liver fibrosis.

XX

Hepatitis C virus.

OS

Hepatitis C virus.

XX

W02003051912-A2.

PN

XX

PD

26-JUN-2003.

XX

18-DEC-2002; 2002WO-EP014480.

XX

18-DEC-2001; 2001US-00020510.

PR

16-OCT-2002; 2002US-0418358P.

XX

(INNO-) INNOCENTIQUES NV.

PA

Maertens G, Depta E, Bosman F;

XX

WPI; 2003-51632/51.

DR

N-PSDB; ADD5513.

New hepatitis C virus (HCV) vaccine composition, useful for reducing liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.

XX

Disclosure; SEQ ID NO 6; 271pp; English.

PS

The invention comprises an Hepatitis C virus (HCV) vaccine for reducing liver disease. The vaccine of the invention comprises an HCV E1 or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present amino acid sequence represents an HCV E1 protein.

XX

Sequence 263 AA;

Query Match 100.0%; Score 185; DB 7; Length 263;

Best Local Similarity 100.0%; Pred. No. 1e-19; Mismatches 34; Conservative 0; Indels 0; Gaps 0;

CC -infected mammal, particularly human. The HCV E1 proteins are useful for
 CC *in vitro* monitoring HCV disease or prognosis the response to treatment
 CC of patients suffering from HCV infection. The present sequence is an HCV
 CC E1 protein (or fragment).

XX SQ Sequence 263 AA;

RESULT 21

AAO18678 100.0%; Score 185; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1e-19; Matches 34; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPHRITGHRMAMDMAMNSPTTALVVSQRLI 34
 ID AAO18678; Standard; protein; 692 AA.
 XX AAC18678;
 XX DT 24-OCT-2002 (first entry)
 DE Hepatitis C virus E2 protein related protein SEQ ID NO: 48.
 XX Hepatitis C virus; HCV; E1 protein; E2 protein; infection; virucide;
 XX immunostimulant; vaccine.
 XX OS Hepatitis C virus.
 XX PN WO200255548-A2.
 XX PD 18-JUL-2002.
 XX PR 11-JAN-2002; 2002WO-EP000219.
 XX PR 11-JAN-2001; 2001US-0265669P.
 XX PR 30-AUG-2001; 2001US-0315768P.
 PA (INNO-) INNOGENETICS NV.
 XX PI Maertens G, Bosman F, Buyse M;
 XX DR WPI: 2002-596657/64.
 XX DR N-PSDB; RAL48939.

XX PT New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific Oligomeric recombinant envelope protein E1 or E2, useful for immunizing humans from HCV infection.

XX PS Disclosure; Page 209-211; 243PP; English.

CC The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for *in vitro* monitoring of HCV disease or prognosis the response to treatment of patients suffering from HCV infection. The present sequence is a protein described in the exemplification of the invention

XX Sequence 692 AA;

XX
XX
DT 24-OCT-2002 (first entry)
DE Hepatitis C virus E2 protein related protein SEQ ID NO: 50.
XX
KW Hepatitis C virus; HCV; E1 protein; E2 protein; infection; virucide;
KW immunostimulant; vaccine.
XX
OS Hepatitis C virus.
XX
PN WO20025548-A2.
XX
PD 18-JUL-2002.
XX
PP 11-JAN-2002; 2002WO-EP000219.
XX
PT 11-JAN-2001; 2001US-0260669P.
PR 30-AUG-2001; 2001US-0315768P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PT Maertens G, Bosman F, Buyse M;
XX
DR WPI; 2002-599657/64.
N-PSDB; AAI48940.
XX
PT New therapeutic vaccine compositions comprising at least one purified
recombinant hepatitis C virus (HCV) single or specific oligomeric
recombinant envelope protein E1 or E2, useful for immunizing humans from
HCV infection.
XX
PS Disclosure; Page 215-218; 243pp; English.
XX
CC The present invention relates to new therapeutic vaccine compositions for
inducing hepatitis C virus (HCV) specific antibodies, comprising a
composition containing at least one purified recombinant HCV single or
specific oligomeric recombinant envelope proteins selected from an E1 and
an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are
useful for inducing HCV-specific antibodies or for immunising humans
against HCV. The recombinant HCV E1 and/or E2 proteins are useful as
vaccines or therapeutics, in HCV screening and confirmatory antibody
tests, for raising antibodies, in the preparation of medicament, and for
in vitro monitoring of HCV disease or prognosis the response to
treatment of patients suffering from HCV infection. The present sequence
CC is a protein described in the exemplification of the invention
XX
SQ Sequence 809 AA;

Query Match 100.0%; Score 185; DB 5; Length 809;
Best Local Similarity 100.0%; Pred. No. 3.7e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIVPGHITGHRMAWDMMNNSPTTALVSQLRI 340
Db 307 SIVPGHITGHRMAWDMMNNSPTTALVSQLRI 340

RESULT 26
ID ADP71140
XX
AC ADP71140;
XX
DT 23-SEP-2004 (first entry)
XX
DE HCV E1 protein HCC166.
XX
KW Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
KW liver disease; liver fibrosis; immunogen; serum alanine aminotransferase level; steatosis;
KW anti-E2 immunoreactivity; vaccine.
XX
OS Hepatitis C virus.
XX
PN US2004126395-A1.
XX
PD 01-JUL-2004.
XX
PP 18-DEC-2002; 2002US-00321798.
XX
PR 18-DEC-2001; 2001US-0453108P.
PR 16-OCT-2002; 2002US-0418358P.
XX
PA (MAER/) MAERTENS G.
PA (DEPL/) DEPLA E.
PA (BOSM/) BOSMAN F.
XX
PT Maertens G, Depla E, Bosman F;
XX
DR WPI; 2004-49909/47.
N-PSDB; ADP71139.
XX
PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver

XX
XX
PD 26-JUN-2003.
XX
PP 18-DEC-2002; 2002WO-EP014480.
XX
PR 18-DEC-2001; 2001US-00020510.
PR 16-OCT-2002; 2002US-0418358P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PT Maertens G, Depla E, Bosman F;
XX
DR WPI; 2003-541632/51.
N-PSDB; ADD5557.
XX
PT New hepatitis C virus (HCV) vaccine composition, useful for reducing
liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
XX
PS Disclosure; SEQ ID NO 50; 271pp; English.
CC The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
CC liver disease. The vaccine of the invention comprises an HCV E1 or E2
CC protein as an antigen. The HCV vaccine is useful for reducing liver
CC disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
CC present amino acid sequence represents an HCV E1/E2 protein.
XX
SQ Sequence 809 AA;

Query Match 100.0%; Score 185; DB 7; Length 809;
Best Local Similarity 100.0%; Pred. No. 3.7e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIVPGHITGHRMAWDMMNNSPTTALVSQLRI 340
Db 307 SIVPGHITGHRMAWDMMNNSPTTALVSQLRI 340

RESULT 26
ID ADP71140
XX
AC ADP71140;
XX
DT 23-SEP-2004 (first entry)
XX
DE HCV E1 protein HCC166.
XX
KW Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
KW liver disease; liver fibrosis; immunogen; serum alanine aminotransferase level; steatosis;
KW anti-E2 immunoreactivity; vaccine.
XX
OS Hepatitis C virus.
XX
PN US2004126395-A1.
XX
PD 01-JUL-2004.
XX
PP 18-DEC-2002; 2002US-00321798.
XX
PR 18-DEC-2001; 2001US-0453108P.
PR 16-OCT-2002; 2002US-0418358P.
XX
PA (MAER/) MAERTENS G.
PA (DEPL/) DEPLA E.
PA (BOSM/) BOSMAN F.
XX
PT Maertens G, Depla E, Bosman F;
XX
DR WPI; 2004-49909/47.
N-PSDB; ADP71139.
XX
PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver

RESULT 25
ADD5558
ID ADD5558 standard; protein; 809 AA.
XX
AC ADD5558;
XX
DT 15-JAN-2004 (first entry)
XX
DE Hepatitis C virus E1/E2 protein #14.
XX
KW Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
KW liver fibrosis.
OS Hepatitis C virus.
XX
PN WO2003051912-A2.

PT disease, serum alanine aminotransferase levels, steatosis, or anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal.

XX

XX CC The invention relates to the use of a hepatitis C virus (HCV) vaccine

XX CC composition for reducing liver disease (such as liver fibrosis or its

XX CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or

XX CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,

XX CC or for treating a chronic HCV-infected mammal. The liver disease is

XX CC reduced by at least 1-2 points according to the overall Ishak score in

XX CC the HCV-infected mammal. Also included are a method for predicting

XX CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic

XX CC HCV vaccine composition (comprising at least one purified or a

XX CC combination of at least 2 HCV single or specific oligomeric recombinant

XX CC envelope proteins selected from an E1 or E2 protein, a part of E1 and E2

XX CC proteins, an E1/E2 protein complex formed from purified HCV single or

XX CC specific oligomeric recombinant E1 or E2 proteins or its parts and

XX CC optionally a pharmaceutical adjuvant), a composition (comprising at least

XX CC one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an

XX CC immunogenic HCV composition (or HCV vaccine composition) comprising a

XX CC recombinant virus allowing expression of at least one HCV recombinant

XX CC envelope protein (selected from an E1 protein and/or an E2 protein, and

XX CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV

XX CC vaccine composition (comprising a recombinant virus allowing expression

XX CC of at least one HCV recombinant envelope protein chosen from an E1

XX CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,

XX CC optionally, a pharmaceutical adjuvant. The HCV vaccine composition is

XX CC used for reducing liver disease (such as liver fibrosis or its

XX CC progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in

XX CC the liver of a chronic HCV-infected mammal, or for treating a chronic HCV

XX CC -infected mammal, particularly human. The HCV E1 proteins are useful for

XX CC in vitro monitoring HCV disease or prognosis the response to treatment

XX CC of patients suffering from HCV infection. The present sequence is an HCV

XX CC E1 protein (or fragment).

SQ Sequence 809 AA:

Query Match	100.0%	Score	185	DB	8	length	809
Best Local Similarity	100.0%	Pred. No.	3	-7e-19			
Matches	34	Conservative	0	Mismatches	0	Indels	0
QY	1	SIYPGHITGHMMAWMDDMMANWSPTTAUJVSQI	34				
Db	307	SIYPGHITGHMMAWMDDMMANWSPTTAUJVSQI	340				

RESULT 27

ID	AAR69647	standard; protein; 192 AA.
XX	XX	
AC	AC	
XX	XX	
DT	DT	
25-MAR-2003	(revised)	
14-SEP-1995	(first entry)	
DB	DB	
Hepatitis C virus envelope 1 protein isolate HK5.		
XX		
XX		
KM	Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate HK5;	
KW	diagnosis; vaccines; antibodies; antisera; gene inhibition.	
OS	Hepatitis C virus.	
XX		
PN	WO9501442-A2.	
XX		
PP	28-JUN-1994; 94WO-US07320.	
XX		
PD	12-JAN-1995.	
XX		
PR	29-JUN-1993; 93US-00086428.	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX		

PI Bukh J, Miller RH, Purcell RH;
 XX DR WPI; 1995-061006/08.
 XX N-PSDB; AAC83859.
 PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
 PT nucleotide(s), peptide(s) and proteins, used in diagnosis and in
 PT vaccines.
 XX
 PS Claim 3; Page 90; 186PP; English.
 XX
 CC AAQ83859 encodes **AAR9647** hepatitis C virus (HCV) envelope 1 (E1) protein
 CC isolate HK5, both can be used for the diagnosis of HCV infection, and in
 CC the produc. of anti-HCV vaccines, antibodies and antisera. The cDNA may
 CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
 CC -MAR-2003 to correct PN field.)
 XX
 SQ Sequence 192 AA;
 Query Match 99.5%; Score 184; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. 9.8e-20; Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIVPGHGTGHRMADMNANWSPTTALVNSQRLI 34
 116 SIVPGHVTGHRMADMNANWSPTTALVNSQRLI 149
 DB

XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
 XX PT determine HCV genotype and as vaccines against HCV infection.
 XX
 PS Claim 2; Page 116; 340pp; English.
 XX
 CC AAR89505-R8955 are HCV E1 (envelope-1) proteins derived from 51 HCV
 CC isolates. Isolated cDNA sequences are used for the prodn. of primers
 CC useful for detecting the presence of HCV in a sample, the primers are
 CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
 CC in vaccines for immunising against HCV infection. The proteins may also
 CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
 CC other mononuclear cells. The antibodies may be used in the prevention of
 CC HCV infection
 XX
 SQ Sequence 192 AA:
 XX
 Query Match 99.5%; Score 184; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 9; 8e-20; 0; Mismatches 0; Indels 0; Gaps 0
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0
 QY 1 SIYPGSHITGHMADMNMNNSPITALVVSQRLI 34
 DB 116 SIYPGSHITGHMADMNMNNSPITALVVSQRLI 149

RESULT 32
 AAR89523 99.5%; Score 184; DB 2; Length 192;
 ID AAR89523 standard; protein; 192 AA.
 XX
 AC AAR89523;
 XX
 DT 30-SEP-1996 (first entry)
 XX
 DE Hepatitis C virus isolate S9 envelope 1 protein.
 XX
 KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
 XX hepatitis.
 OS Hepatitis C virus.
 XX
 PN WO9605315-A2.
 XX
 PD 22-FEB-1996.
 XX
 PF 15-AUG-1995; 95WO-US010398.
 PR 15-AUG-1994; 94US-00290665.
 XX
 PA (USSH) US SEC DEPT HEALTH.
 XX
 PI Bukh J, Miller RH, Purcell RH;
 XX
 DR WPI; 1996-139709/14.
 XX
 DR N-PSDB; AARI6577.
 XX
 PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
 XX determine HCV genotype and as vaccines against HCV infection.
 XX
 PS Claim 2; Page 124; 340pp; English.
 XX
 CC AAR89505-R8955 are HCV E1 (envelope-1) proteins derived from 51 HCV
 CC isolates. Isolated cDNA sequences are used for the prodn. of primers
 CC useful for detecting the presence of HCV in a sample, the primers are
 CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
 CC in vaccines for immunising against HCV infection. The proteins may also
 CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
 CC other mononuclear cells. The antibodies may be used in the prevention of
 CC HCV infection
 XX
 Sequence 192 AA;

XX HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
 XX hepatitis.
 XX OS Hepatitis C virus.
 XX
 PN WO9605315-A2.
 XX PD 22-FEB-1996.
 XX PP 15-AUG-1995; 95WO-US010398.
 XX PR 15-AUG-1994; 94US-00230665.
 XX PA (USSH) US SEC DEPT HEALTH.
 XX PI Buhk J, Miller RH, Purcell RH;
 XX DR WPI; 1996-139709/14.
 XX DR N-PSDB; AATI6572.
 XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
 determine HCV genotype and as vaccines against HCV infection.
 XX PS Claim 2, Page 120, 340pp, English.
 XX ARB89505-R89555 are HCV E1 (envelope-1) proteins derived from 51 HCV
 isolates. Isolated cDNA sequences are used for the prodn. of primers
 useful for detecting the presence of HCV in a sample, the primers are
 also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
 in vaccines for immunising against HCV infection. The proteins may also
 be used to detect antibodies against HCV in serum, saliva, lymphocytes or
 other mononuclear cells. The antibodies may be used in the prevention of
 HCV infection
 XX SQ Sequence 192 AA;
 XX Query Match 99.5%; Score 184; DB 2; Length 192;
 XX Best Local Similarity 97.1%; Pred. No. 9.8e-20; 0; Mismatches 1; Indels 0; Gaps 0;
 XX Matches 33; Conservative 1; QY 1 SIVPGHHTCHRMADMDDMMWSPTPAVLSQLRI 34
 XX Db 116 SIVPGHHTCHRMADMDDMMWSPTPAVLSQLRI 149
 XX
 RESULT 35
 AAB18532
 ID AAB18532 standard; protein; 106 AA..
 XX AC AAB18532;
 XX DT 15-JAN-2001 (first entry)
 XX DE Protein encoded by a novel hepatitis C virus cDNA clone CA156e.
 XX KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
 XX Viral infectivity; viral replication.
 XX OS -Hepatitis C virus.
 XX PN EP1034785-A2.
 XX
 XX 13-SEP-2000.
 XX PP 16-MAR-1990; 2000EP-00109602.
 XX PR 17-MAR-1989; 89US-00325338.
 XX PR 20-APR-1989; 89US-00341334.
 XX PR 18-MAY-1989; 89US-0035002.
 XX PR 16-MAR-1990; 90EP-00302866.
 XX PA (CHIR) CHIRON CORP.

PI Houghton M, Choo Q, Ruo G;
 XX DR
 XX WPI; 2000-566891/53.
 DR N-PSDB; AAA75288.
 XX PT Novel composition comprising a hepatitis C virus antisense polynucleotide
 PT which is complementary to or corresponds to a sense strand of the virus
 PT genome, and selectively hybridizes to it.
 XX PS Example; Fig 8; 75pp; English.
 XX CC The specification describes a pharmaceutical composition which comprises
 CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
 CC characterized by a positive stranded RNA genome which has 40% homology at
 CC the polypeptide level to a HCV polyprotein. The antisense polynucleotide at
 CC birds to cellular polynucleotides which enhance and/or are required for
 CC viral infectivity, replicative ability or chronicity. The antisense
 CC polynucleotides may be designed to bind with high specificity, to be
 CC of increased stability, to be stable and to have low toxicity. The
 CC composition also comprises an agent which causes viral RNA to be
 CC inactive. The composition is used for preventing HCV replication in a
 CC system. The present sequence is encoded by a novel HCV cDNA sequence,
 CC which is used in the course of the invention.
 XX SQ Sequence 106 AA;
 Query Match 98.4%; Score 182; DB 3; Length 106;
 Best Local Similarity 97.1%; Pred. No. 9; e=20;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 AC ID ADN35960;
 XX DT 17-JUN-2004 (first entry)
 XX DB HCV cDNA clone CA156e protein.
 XX KW Antiviral; Vaccine; hepatitis C virus infection; HCV infection.
 XX OS Hepatitis C virus.
 XX PN EP1394255-A2.
 XX PD 03-MAR-2004.
 XX PP 16-MAR-1990; 2003EP-00016585.
 PR 17-MAR-1999; 89US-00325338.
 PR 20-MAR-1989; 89US-00341334.
 PR 18-MAY-1999; 89US-00325002.
 PR 16-MAR-1990; 90EP-00302866.
 XX PA (CHIR) CHIRON CORP.
 XX PI Houghton M, Choo Q, Kuo G;
 XX DR WPI; 2004-193149/19.
 XX DR N-PSDB; ADN35961.
 XX PT Novel purified hepatitis C virus polypeptide comprising epitope encoded
 PT by hepatitis C virus cDNA, useful as vaccine for treating hepatitis C
 virus.
 XX PS Example 1; Fig 8; 79pp; English.

CC The present invention relates to hepatitis C virus (HCV) proteins and
 CC cDNA sequences. The sequences are useful in immunoassays for detecting
 CC antibodies directed against HCV antigen; preparing host cells transformed
 CC with a recombinant polynucleotide; screening antiviral agents and
 CC determining the effect of antiviral agent in inhibiting viral replication
 CC in cell culture system; and developing vaccine for treating HCV
 CC infection.

XX Sequence 106 AA;

Query Match 98.4%; Score 182; DB 8; Length 106;
 Best Local Similarity 97.1%; Pred. No. 9, 9e-20;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SIYPGHTGHRMADMNMNSPTALVVSQI 34
 Db 70 SIYPGHTGHRMADMNMNSPTALVVAQI 103

RESULT 37

AAR69638 ID AAR69638 standard; protein, 192 AA.

AC AAR69638;

XX DT 25-MAR-2003 (revised)
 DT 14-SEP-1995 (first entry)

XX Hepatitis C virus envelope 1 protein isolate SW1.

XX Hepatitis C virus envelope 1 protein isolate SW1.

XX Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate SW1;

XX diagnosis; vaccines; antibodies; antisera; gene inhibition.

XX OS Hepatitis C virus.

XX PN WO9501442-A2.

XX PD 12-JAN-1995.

XX PF 28-JUN-1994; 94WO-US007320.

XX PR 29-JUN-1993; 93US-00086428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Bukh J, Miller RH, Purcell RH;

XX DR WPI: 1995-061006/08.

XX N-PSDB; AAQ83851.

PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-

PT nucleotide(s), peptide(s) and proteins, used in diagnosis and in

PT vaccines.

XX PS claim 3; Page 84-85; 186PP; English.

XX AAQ83851 encodes AAR69640 hepatitis C virus (HCV) envelope 1 (E1) protein
 CC isolate SW1, both can be used for the diagnosis of HCV infection, and in
 CC the produc. of anti-HCV vaccines, antibodies and antisera. The cDNA may
 CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
 CC -MAR-2003 to correct PN field.)

XX Sequence 192 AA;

Query Match 98.4%; Score 182; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 2e-19; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHTGHRMADMNMNSPTALVVSQI 34
 Db 116 SIYPGHTGHRMADMNMNSPTALVVAQI 149

RESULT 39

AAR69634 ID AAR69634 standard; protein, 192 AA.

AC AAR69634;

XX DT 25-MAR-2003 (revised)
 DT 14-SEP-1995 (first entry)

XX Hepatitis C virus envelope 1 protein isolate DR7.

XX Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate DR7;

XX diagnosis; vaccines; antibodies; antisera; gene inhibition.

XX OS Hepatitis C virus.

XX PN WO9501442-A2.

XX PD 12-JAN-1995.

Query Match 98.4%; Score 182; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 2e-19; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHTGHRMADMNMNSPTALVVSQI 34
 Db 116 SIYPGHTGHRMADMNMNSPTALVVAQI 149

XX 28-JUN-1994; 94WO-US007320.
 XX PR 29-JUN-1993; 93US-C0086428.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Bukh J, Miller RH, Purcell RH;
 XX DR WPI; 1995-061006/08.
 XX DR N-PSDB; AAQ83845.
 XX PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
 XX nucleotide(s), peptide(s) and proteins, used in diagnosis and in
 XX vaccines.
 XX PS Claim 3; Page 80; 186PP; English.
 XX CC AAQ83845 encodes AAR69634 hepatitis C virus (HCV) envelope 1 (E1) protein
 CC isolate DK7, both can be used for the diagnosis of HCV infection, and in
 CC the produc. of anti-HCV vaccines, antibodies and antisera. The cDNA may
 CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
 CC -MAR-2003 to correct PN field.)
 XX PS Sequence 192 AA;
 XX Query Match 98.4%; Score 182; DB 2; Length 192;
 XX Best Local Similarity 97.1%; Pred. No. 2e-19;
 XX Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 SIYPGHTGHRMADMNMWSPTTALVWSQIRI 34
 DB 116 SIYPGHTGHRMADMNMWSPTTALVWSQIRI 149
 RESULT 40
 XX AAR69637
 XX ID AAR69637 standard; protein; 192 AA.
 XX AC AAR69637;
 XX DT 25-MAR-2003 (revised)
 XX DT 14-SEP-1995 (first entry)
 DE Hepatitis C virus envelope 1 protein isolate DR4.
 DE Hepatitis C virus envelope 1 protein isolate DR4.
 XX Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate DR4;
 XX diagnosis; vaccines; antibodies; antisera; gene inhibition.
 OS Hepatitis C virus.
 OS Hepatitis C virus.
 PN WO9501442-A2.
 XX PR 12-JAN-1995.
 XX PD 28-JUN-1994; 94WO-US007320.
 XX PR 29-JUN-1993; 93US-00086428.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PT PI Bukh J, Miller RH, Purcell RH;
 XX DR WPI; 1995-061006/08.
 XX DR N-PSDB; AAQ83848.
 XX PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
 PT nucleotide(s), peptide(s) and proteins, used in diagnosis and in
 PT vaccines.
 XX PS Claim 3; Page 81-82; 186PP; English.
 XX CC AAQ83848 encodes AAR69637 hepatitis C virus (HCV) envelope 1 (E1) protein

CC isolate DR4, both can be used for the diagnosis of HCV infection, and in
 CC the produc. of anti-HCV vaccines, antibodies and antisera. The cDNA may
 CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
 CC -MAR-2003 to correct PN field.)
 XX Sequence 192 AA;
 XX Search completed: November 10, 2004, 18:14:36
 Job time : 158 secs
 Query Match 98.4%; Score 182; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 2e-19;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHTGHRMADMNMWSPTTALVWSQIRI 34
 Db 116 SIYPGHTGHRMADMNMWSPTTALVWSQIRI 149

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OM protein - protein search, using sw model

Run on: November 10, 2004, 18:09:29 ; Search time: 38 seconds
(without alignments)
59.337 Million cell updates/sec

Title: US-10-685-435-15
Perfect score: 185
Sequence: 1 SIYPGHTGHRMAWDMNNWSPTTALVSQLRI 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 47139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/pcnUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/packfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	185	100.0	34	US-09-645-470-6
2	185	100.0	34	US-09-355-440-23
3	185	100.0	139	US-08-444-818-173
4	185	100.0	200	US-08-612-973-25
5	185	100.0	200	US-08-927-597-26
6	185	100.0	210	US-08-612-973-28
7	185	100.0	210	US-08-927-597-28
8	185	100.0	212	US-08-612-973-4
9	185	100.0	212	US-08-927-597-4
10	185	100.0	239	US-08-612-973-22
11	185	100.0	239	US-08-927-597-22
12	185	100.0	263	US-08-612-973-6
13	185	100.0	263	US-08-927-597-6
14	185	100.0	692	US-08-612-973-48
15	185	100.0	692	US-08-927-597-48
16	185	100.0	809	US-08-612-973-50
17	185	100.0	809	US-08-927-597-50
18	184	99.5	192	US-08-612-973-60
19	184	99.5	192	US-08-612-973-65
20	184	99.5	192	US-08-086-428B-70
21	184	99.5	192	US-08-086-428B-74
22	184	99.5	192	US-08-468-570-60
23	184	99.5	192	US-08-468-570-65
24	184	99.5	192	US-08-468-570-70
25	184	99.5	192	US-08-468-570-74
26	184	99.5	192	US-08-290-665A-60
27	184	99.5	192	US-08-290-665A-65

ALIGNMENTS

RESULT 1
US-09-645-470-6
; Sequence 6, Application US/09645470
; Patent No. 6521403

; GENERAL INFORMATION:
; APPLICANT: MARTENS, GEERT
; APPLICANT: DELTA, ERIK
; APPLICANT: BUXSE, MARIE-ANGE
; TITLE OF INVENTION: BIOTYPES IN VIRAL ENVELOPE PROTEINS AND SPECIFIC
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST THESE BIOTYPES: USE FOR
; TITLE OF INVENTION: DETECTION OF HCV VIRAL ANTIGEN IN HOST TISSUE
; FILE REFERENCE: 2551-47
; CURRENT APPLICATION NUMBER: US/09-645, 470
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/EP99/02154
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-645-470-6

Query Match Score: 100.0%; Score: 185; DB: 4; Length: 34;
Best Local Similarity: 100.0%; Pred. No. 5.5e-20;
Matches: 34; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 SIYPGHTGHRMAWDMNNWSPTTALVSQLRI 34
Dy 1 SIYPGHTGHRMAWDMNNWSPTTALVSQLRI 34

RESULT 2
US-09-55-040-23
; Sequence 23, Application US/09355040
; Patent No. 663257

; GENERAL INFORMATION:
; APPLICANT: MARTENS, GEERT
; APPLICANT: DELTA, ERIK
; APPLICANT: BOSMAN, ALFONS
; APPLICANT: VAN WIJENDALE, FRANS
; TITLE OF INVENTION: PARTICLES OF HCV ENVELOPE PROTEINS: USE FOR VACCINATION
; FILE REFERENCE: Delta
; CURRENT APPLICATION NUMBER: US/09/355, 040
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: PCT/EP99/04342
; EARLIER FILING DATE: 1999-06-23

Sequence 70, Appl
Sequence 74, Appl
Sequence 60, Appl
Sequence 65, Appl
Sequence 74, Appl
Sequence 70, Appl
Sequence 60, Appl
Sequence 65, Appl
Sequence 74, Appl
Sequence 70, Appl
Sequence 60, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 58, Appl

EARLIER APPLICATION NUMBER: EP 98870142.1
 EARLIER FILING DATE: 1998-02-24
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 23
 LENGTH: 34
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-09-355-040-23

RESULT 3
 US-08-444-818-173
 Sequence 173, Application US/08444818
 Patent No. 615087
 GENERAL INFORMATION:
 APPLICANT: Chien, David Y.
 TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 NUMBER OF SEQUENCES: 777
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 ZIP: 94608-916
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,973
 FILING DATE: 11-MAR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 amino acid
 TYPE: amino acid
 TOPLOGY: linear
 MOLECULE TYPE: protein
 US-08-612-973-26

Query Match 100.0%; Score 185; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.5e-20; Mismatches 0;
 Matches 34; Conservative 0; Indels 0; Gaps 0;
 QY 1 STYPGHTGHRNAWMNMNSPTTALVVSQQLRI 34
 Db 1 SIYPGHTGHRNAWMNMNSPTTALVVSQQLRI 34

RESULT 4
 US-08-612-973-26
 Sequence 26, Application US/08612973
 Patent No. 615013
 GENERAL INFORMATION:
 APPLICANT: MAERTENS, GEERT
 APPLICANT: BOSMAN, FONS
 APPLICANT: DE MARTYNOFF, GUY
 APPLICANT: BUYSE, MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,973
 FILING DATE: 11-MAR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 199:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 amino acid
 TYPE: amino acid
 TOPLOGY: linear
 MOLECULE TYPE: protein
 US-08-612-973-26

Query Match 100.0%; Score 185; DB 3; Length 200;
 Best Local Similarity 100.0%; Pred. No. 4.2e-19; Mismatches 0;
 Matches 34; Conservative 0; Indels 0; Gaps 0;
 QY 1 STYPGHTGHRNAWMNMNSPTTALVVSQQLRI 34
 Db 1 166 SIYPGHTGHRNAWMNMNSPTTALVVSQQLRI 199

RESULT 5
 US-08-927-597-26
 Sequence 26, Application US/08927597
 Patent No. 6245503
 GENERAL INFORMATION:
 APPLICANT: MAERTENS, GEERT
 APPLICANT: BOSMAN, FONS
 APPLICANT: DE MARTYNOFF, GUY
 APPLICANT: BUYSE, MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.

RESULT 3
 US-08-444-818-173
 Sequence 173, Application US/08444818
 Patent No. 615087
 GENERAL INFORMATION:
 APPLICANT: Chien, David Y.
 TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 NUMBER OF SEQUENCES: 777
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 ZIP: 94608-916
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,973
 FILING DATE: 11-MAR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 amino acid
 TYPE: amino acid
 TOPLOGY: linear
 MOLECULE TYPE: protein
 US-08-612-973-26

Query Match 100.0%; Score 185; DB 3; Length 139;
 Best Local Similarity 100.0%; Pred. No. 2.8e-19; Mismatches 0;
 Matches 34; Conservative 0; Indels 0; Gaps 0;
 QY 1 SIYPGHTGHRNAWMNMNSPTTALVVSQQLRI 34
 Db 1 |||||SIYPGHTGHRNAWMNMNSPTTALVVSQQLRI 34

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/403,590
 FILING DATE: 14-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Harbin, Alisa A.
 REGISTRATION NUMBER: 33,825
 REFERENCE DOCKET NUMBER: 0110.002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508) 359-3876
 TELEFAX: (508) 359-3885
 INFORMATION FOR SEQ ID NO: 173:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 139 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE: INDIVIDUAL ISOLATE: Japanese isolate (T. Miyamura)
 ; US-08-444-818-173

SEQUENCE CHARACTERISTICS:
 LENGTH: 210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-612-973-28

Query Match 100.0%; Score 185; DB 3; Length 210;
 Best Local Similarity 100.0%; Pred. No. 4.4e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIVPGHITGHRMADMNNWSPTALVVSQRLI 34
 Do 166 SIVPGHITGHRMADMNNWSPTALVVSQRLI 199

RESULT 7
 US-08-927-597-28
 ; Sequence 28, Application US/08927597
 ; Patent No. 6245503
 ; GENERAL INFORMATION:
 ; APPLICANT: MAERENS, GEERT
 ; APPLICANT: BOSMAN, FONS
 ; APPLICANT: DE MARTINOFF, GUY
 ; APPLICANT: BUYSE, MARIE ANGE
 ; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 ; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
 ; NUMBER OF SEQUENCES: 111
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHVE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/612,973
 FILING DATE: 11-MAR-1996
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/927,597
 FILING DATE:
 CLASSIFICATION:
 REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:
 LENGTH: 210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-927-597-28

Query Match 100.0%; Score 185; DB 3; Length 210;
 Best Local Similarity 100.0%; Pred. No. 4.4e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIVPGHITGHRMADMNNWSPTALVVSQRLI 34
 Do 166 SIVPGHITGHRMADMNNWSPTALVVSQRLI 199

RESULT 8
 US-08-612-973-4

Sequence 4, Application US/08612973
 Patent No. 6150134
 GENERAL INFORMATION:
 APPLICANT: MAERTENS, GEERT
 APPLICANT: BOSMAN, FONS
 APPLICANT: DE MARTYNOFF, GUY
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,973
 FILING DATE: 11-MAR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 Qy 1 SIYPGHITGRMADMNNWSPTALVSQLRI 34
 Db 139 SIYPGHITGRMADMNNWSPTALVSQLRI 172
 RESULT 9
 Query Match 100.0%; Score 185; DB 3; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SIYPGHITGRMADMNNWSPTALVSQLRI 34
 Db 139 SIYPGHITGRMADMNNWSPTALVSQLRI 172
 RESULT 9
 Sequence 4, Application US/08927597
 Patent No. 6245503
 GENERAL INFORMATION:
 APPLICANT: MAERTENS, GEERT
 APPLICANT: BOSMAN, FONS
 APPLICANT: DE MARTYNOFF, GUY
 APPLICANT: BUYSE, MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,973
 FILING DATE: 11-MAR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 239 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-927-597-4
 Sequence 10
 Query Match 100.0%; Score 185; DB 3; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SIYPGHITGRMADMNNWSPTALVSQLRI 34
 Db 139 SIYPGHITGRMADMNNWSPTALVSQLRI 172
 RESULT 10
 Sequence 22, Application US/08612973
 Patent No. 6150134
 GENERAL INFORMATION:
 APPLICANT: MAERTENS, GEERT
 APPLICANT: BOSMAN, FONS
 APPLICANT: DE MARTYNOFF, GUY
 APPLICANT: BUYSE, MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 NUMBER OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,973
 FILING DATE: 11-MAR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 239 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-612-973-22

Query Match 100.0%; Score 185; DB 3; Length 239;
 Best Local Similarity 100.0%; Pred. No. 5.1e-19; Mismatches 0;
 Matches 34; Conservative 0; Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMMNNWSPTALVSQLRI 34
 Db 166 SIYPGHTGHRMADMMNNWSPTALVSQLRI 199

RESULT 11

US-08-927-597-22
 ; Sequence 22, Application US/08927597
 ; Patent No. 6245503

GENERAL INFORMATION:
 APPLICANT: MAERTENS, GEERT

APPLICANT: BOSMAN, FONS

APPLICANT: DE MARTYNOFF, GUY

APPLICANT: BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111
 NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,973

FILING DATE: 11-MAR-1996

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

APPLICATION NUMBER: US 08/612,973

FILING DATE:

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 6:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/612,973
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 815-4100
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 263 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-927-597-6

Query Match 100.0%; Score 185; DB 3; Length 263;
 Best Local Similarity 100.0%; Pred. No. 5.7e-19; Mismatches 0;
 Matches 34; Conservative 0; Indels 0; Gaps 0;
 QY 1 SIVPGHTGHRMWDMMNNWSPTALVSQLRI 34
 Db 190 SIVPGHTGHRMWDMMNNWSPTALVSQLRI 223

RESULT 14

US-08-612-973-48

Sequence 48 Application US/08927597
 Patent No. 6245503
 GENERAL INFORMATION:
 APPLICANT: MARTEENS, GEERT

APPLICANT: BOSMAN, FONS
 APPLICANT: DE MARTYNOFF, GUY
 APPLICANT: BUJSE, MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/927,597
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 692 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-927-597-48

Query Match 100.0%; Score 185; DB 3; Length 692;
 Best Local Similarity 100.0%; Pred. No. 1.7e-18; Mismatches 0;
 Matches 34; Conservative 0; Indels 0; Gaps 0;

QY 1 SIVPGHTGHRMWDMMNNWSPTALVSQLRI 34
 Db 190 SIVPGHTGHRMWDMMNNWSPTALVSQLRI 223

RESULT 15

Sequence 48 Application US/08927597
 Patent No. 6245503
 GENERAL INFORMATION:
 APPLICANT: MARTEENS, GEERT

APPLICANT: BOSMAN, FONS
 APPLICANT: DE MARTYNOFF, GUY
 APPLICANT: BUJSE, MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/927,597
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 692 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-612-973-48

Query Match 100.0%; Score 185; DB 3; Length 692;
 Best Local Similarity 100.0%; Pred. No. 1.7e-18; Mismatches 0;
 Matches 34; Conservative 0; Indels 0; Gaps 0;

QY 1 SIVPGHTGHRMWDMMNNWSPTALVSQLRI 34
 Db 190 SIVPGHTGHRMWDMMNNWSPTALVSQLRI 223

RESULT 16

Sequence 50 Application US/08612973
 Patent No. 6150134
 GENERAL INFORMATION:
 APPLICANT: MARTEENS, GEERT

APPLICANT: BOSMAN, FONS
 APPLICANT: DE MARTYNOFF, GUY
 APPLICANT: BUJSE, MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/927,597
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 692 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-612-973-48

Query Match 100.0%; Score 185; DB 3; Length 692;
 Best Local Similarity 100.0%; Pred. No. 1.7e-18; Mismatches 0;
 Matches 34; Conservative 0; Indels 0; Gaps 0;

QY 1 SIVPGHTGHRMWDMMNNWSPTALVSQLRI 34
 Db 190 SIVPGHTGHRMWDMMNNWSPTALVSQLRI 223

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHVE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,973

FILING DATE: 11-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 11487-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 809 amino acids

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 809 amino acids

TYPE: amin acid

TOPOLogy: linear

MOLECULE TYPE: protein

US-08-927-597-50

RESULT 17

US-08-927-597-50

Sequence 50, Application US/08927597

Patent No. 6445503

GENERAL INFORMATION:

APPLICANT: MAARTENS, GEERT

APPLICANT: BOSMAN, FONS

APPLICANT: DE MARTINOFF, GUY

APPLICANT: BYUSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHVE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/927,597

FILING DATE: 11-MAR-1996

CLASSIFICATION: 435

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLogy: unknown

ORIGINAL SOURCE:

ORGANISM: homosapiens

INDIVIDUAL ISOLATE: D1

US-08-086-428B-60

Query Match:

Best Local Similarity 97.1%; Pred. No. 5,6e-19;

Matches 33; Conservative 1; MisMatches 0; Indels 0; Gaps 0;

REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 809 amino acids
TYPE: amino acid
TOPOLogy: linear
MOLECULE TYPE: protein
US-08-927-597-50RESULT 18
US-08-086-428B-60
Sequence 60, Application US/08086428B
Patent No. 551539
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R. H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF PROTEINS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154RESULT 18
US-08-086-428B-60
Sequence 60, Application US/08086428B
Patent No. 551539
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R. H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF PROTEINS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLogy: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: D1
US-08-086-428B-60Query Match:
Best Local Similarity 97.1%; Pred. No. 5,6e-19;
Matches 33; Conservative 1; MisMatches 0; Indels 0; Gaps 0;

QY 1 SYPGHTGHRMADMAMNSPTALVSQLRI 34
 DB 116 SYPGHTGHRMADMAMNSPTALVSQLRI 149

RESULT 19

US-08-085-428B-65

Sequence 65, Application US/08086428B

Patent No. 5514539

GENERAL INFORMATION:

APPLICANT: BURK, J., MILLER, R.H. AND

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE

TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE

TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN

TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES

NUMBER OF SEQUENCES: 159

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/086,428B

FILING DATE: 29-JUN-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK

REGISTRATION NUMBER: 35,459

REFERENCE/DOCKET NUMBER: 2026-4070

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 751-4000

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

ORIGINAL SOURCE:

ORGANISM: homosapiens

INDIVIDUAL ISOLATE: S9

US-08-086-428B-70

Query Match 99.5%; Score 184; DB 1; Length 192;
 Best Local Similarity 97.1%; Pred. No. 5.6e-19;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-08-086-428B-74

Query Match 99.5%; Score 184; DB 1; Length 192;
 Best Local Similarity 97.1%; Pred. No. 5.6e-19;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-08-086-428B-74

Sequence 74, Application US/08086428B

Patent No. 5514539

GENERAL INFORMATION:

APPLICANT: BURK, J., MILLER, R.H. AND

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE

TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE

TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN

TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES

NUMBER OF SEQUENCES: 159

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/086,428B

FILING DATE: 29-JUN-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK

REFERENCE/DOCKET NUMBER: 36,459

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: 421792

TELEX: 421792

INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:

SEQUENCE: 192 amino acids

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

ORIGINAL SOURCE:

ORGANISM: homosapiens

INDIVIDUAL ISOLATE: D1

US-08-468-570-60

Query Match 99.5%; Score 184; DB 1; Length 192;

Best Local Similarity 97.1%; Pred. No. 5.6e-19; Mismatches 0; Indels 0; Gaps 0;

Matches 33; Conservative 1; MisMatches 0; Indels 0; Gaps 0;

Qy 1 SIVPGHITGRHMAWDMMNNNSPTALVVSQQLRI 34

Db 116 SIVPGHITGRHMAWDMMNNNSPTALVVSQQLRI 149

Query Match 99.5%; Score 184; DB 2; Length 192;

Best Local Similarity 97.1%; Pred. No. 5.6e-19; Mismatches 0; Indels 0; Gaps 0;

Matches 33; Conservative 1; MisMatches 0; Indels 0; Gaps 0;

Qy 1 SIVPGHITGRHMAWDMMNNNSPTALVVSQQLRI 34

Db 115 SIVPGHITGRHMAWDMMNNNSPTALVVSQQLRI 149

RESULT 23

US-08-468-570-65

Sequence 65, Application US/08468570

GENERAL INFORMATION:

APPLICANT: BURKH, J., MILLER, R.H. AND

APPLICANT: PURCELL, R.H.

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE

TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE

TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN

TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN

TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES

NUMBER OF SEQUENCES: 159

NUMBER OF SEQUENCES: 159

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,570

FILING DATE: 6-JUN-1995

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/086,428

FILING DATE: 29-JUN-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK

REGISTRATION NUMBER: 36,459

REFERENCE/DOCKET NUMBER: 2026-4070US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

SEQUENCE: 192 amino acids

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

ORIGINAL SOURCE:

ORGANISM: homosapiens

INDIVIDUAL ISOLATE: HKS

US-08-468-570-65

Query Match 99.5%; Score 184; DB 2; Length 192;

Best Local Similarity 97.1%; Pred. No. 5.6e-19;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYPGHTGHRMADMNNWSPTALVSQLRI 34
 Best Local Similarity 97.1%; Pred. No. 5.6e-19; Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 116 SYPGHTGHRMADMNNWSPTALVSQLRI 149

RESULT 24
 US-08-468-570-70
 Sequence 70, Application US/08468570
 Patent No. 5871962
 GENERAL INFORMATION:
 APPLICANT: BURKH, J., MILLER, R.H. AND
 APPLICANT: PURCELL, R.H.
 TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE OF 51 ISOLATES OF HEPATITIS C AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
 NUMBER OF SEQUENCES: 159
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,570
 FILING DATE: 6-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/086,428
 FILING DATE: 29-JUN-1993
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: RICHARD W. BORK
 REGISTRATION NUMBER: 35,459
 REFERENCE/DOCKET NUMBER: 2025-4070US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 751-4100
 TELEFAX: (212) 751-6849
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 74:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 ORIGINAL SOURCE:
 ORGANISM: homosapiens
 INDIVIDUAL ISOLATE: T3
 US-08-468-570-74
 RESULT 25
 Query Match 99.5%; Score 184; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 5.6e-19;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYPGHTGHRMADMNNWSPTALVSQLRI 34
 Db 116 SYPGHTGHRMADMNNWSPTALVSQLRI 149

RESULT 26
 US-08-290-665A-60
 Sequence 60, Application US/08290665A
 Patent No. 5882852
 GENERAL INFORMATION:
 APPLICANT: BURKH, J., MILLER, R.H. AND
 APPLICANT: PURCELL, R.H.
 TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
 NUMBER OF SEQUENCES: 263
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK

RESULT 25
 US-08-468-570-74
 Sequence 74, Application US/08468570
 Patent No. 5871962
 GENERAL INFORMATION:

Best Local Similarity 97.1%; Pred. No. 5.6e-19; Mismatches 1; Indels 0; Gaps 0; Matches 33; Conservative 1; Number of Sequences: 160

RESULT 29
US-08-290-665A-74
Sequence 74, Application US/08290665A
Patent No. 588852
GENERAL INFORMATION:
APPLICANT: BURK, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 35,459
REFERENCE/DOCKET NUMBER: 2026-4070US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4100
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: D1
TELEPHONE: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T3
US-08-290-665A-74

RESULT 30
Query Match 99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19; Mismatches 1; Indels 0; Gaps 0; Matches 33; Conservative 1; Number of Sequences: 160

Query 1 SIVPGHITGHRMADMNNNSPTALVSQLRI 34
DB 116 SIVPGHITGHRMADMNNNSPTALVSQLRI 149

RESULT 31
US-08-466-601A-65
Sequence 65, Application US/08466601A
Patent No. 6572864
GENERAL INFORMATION:
APPLICANT: BURK, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

Best Local Similarity 97.1%; Pred. No. 5.6e-19; Mismatches 1; Indels 0; Gaps 0; Matches 33; Conservative 1; Number of Sequences: 160

Query 1 SIVPGHITGHRMADMNNNSPTALVSQLRI 34
DB 116 SIVPGHITGHRMADMNNNSPTALVSQLRI 149

RESULT 32
US-08-466-601A-60
Sequence 60, Application US/08466601A
Patent No. 6572864
GENERAL INFORMATION:
APPLICANT: BURK, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

Best Local Similarity 97.1%; Pred. No. 5.6e-19; Mismatches 1; Indels 0; Gaps 0; Matches 33; Conservative 1; Number of Sequences: 160

Query 1 SIVPGHITGHRMADMNNNSPTALVSQLRI 34
DB 116 SIVPGHITGHRMADMNNNSPTALVSQLRI 149

RESULT 33
US-08-466-601A-60
Sequence 60, Application US/08466601A
Patent No. 6572864
GENERAL INFORMATION:
APPLICANT: BURK, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

Best Local Similarity 97.1%; Pred. No. 5.6e-19; Mismatches 1; Indels 0; Gaps 0; Matches 33; Conservative 1; Number of Sequences: 160

Query 1 SIVPGHITGHRMADMNNNSPTALVSQLRI 34
DB 116 SIVPGHITGHRMADMNNNSPTALVSQLRI 149

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,601A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/086,428

FILING DATE: 29-JUN-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK

REGISTRATION NUMBER: 36,459

REFERENCE/DOCKET NUMBER: 2026-4070US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-8000

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

ORIGINAL SOURCE:

ORGANISM: homosapiens

INDIVIDUAL ISOLATE: S9

US-08-466-601A-65

Query Match 99.5%; Score 184; DB 4; Length 192;

Best Local Similarity 97.1%; Pred. No. 5.6e-19; Mismatches 0; Indels 0; Gaps 0;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIVPGHITGHRMADMNWNNSPTTALVVSQRLI 34

Db 116 SIVPGHITGHRMADMNWNNSPTTALVVSQRLI 149

RESULT 32

US-08-466-601A-70

Query Match 99.5%; Score 184; DB 4; Length 192;

Best Local Similarity 97.1%; Pred. No. 5.6e-19; Mismatches 0; Indels 0; Gaps 0;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIVPGHITGHRMADMNWNNSPTTALVVSQRLI 34

Db 116 SIVPGHITGHRMADMNWNNSPTTALVVSQRLI 149

RESULT 33

US-08-466-601A-74

Sequence 74, Application US/08466601A

Patent No. 6572864

GENERAL INFORMATION:

APPLICANT: BURKH, J., MILLER, R.H. AND

APPLICANT: PURCELL, R.H.

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE

TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE

TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN

TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES

NUMBER OF SEQUENCES: 160

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,601A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/086,428

FILING DATE: 29-JUN-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK

REGISTRATION NUMBER: 36,459

REFERENCE/DOCKET NUMBER: 2026-4070US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 ORIGINAL SOURCE:
 ORGANISM: homosapiens
 INDIVIDUAL ISOLATE: T3
 US-08-466-601A-74

Query Match 99.5%; Score 184; DB 4; Length 192;
 Best Local Similarity 97.1%; Pred. No. 5.6e-19; Db
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 34 ; PCT-US95-10398-60
 ; Sequence 60, Application PC/TUS9510398
 ; GENERAL INFORMATION:
 ; APPLICANT: BURK, J., MILLER, R.H. AND
 ; APPLICANT: PURCELL, R.H.
 ; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
 ; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
 ; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
 ; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
 ; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
 ; NUMBER OF SEQUENCES: 263
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345, PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT-US95/10398
 ; FILING DATE: 15-AUG-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/086,428
 ; FILING DATE: 29 JUNE 1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/290/665
 ; FILING DATE: 15 AUGUST 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RICHARD W. BORK
 ; REGISTRATION NUMBER: 36,459
 ; REFERENCE/DOCKET NUMBER: 2026-4116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4800
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 65:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 192 amino acids
 ; STRANDEDNESS: amino acid
 ; TOPLOGY: unknown
 ; ORIGINAL SOURCE:
 ; ORGANISM: homosapiens
 ; INDIVIDUAL ISOLATE: HKS
 ; PCT-US95-10398-65

Query Match 99.5%; Score 184; DB 5; Length 192;
 Best Local Similarity 97.1%; Pred. No. 5.6e-19; Db
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 35 ; PCT-US95-10398-65
 ; Sequence 65, Application PC/TUS9510398
 ; GENERAL INFORMATION:
 ; APPLICANT: BURK, J., MILLER, R.H. AND
 ; APPLICANT: PURCELL, R.H.
 ; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
 ; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
 ; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
 ; NUMBER OF SEQUENCES: 263
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345, PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT-US95/10398
 ; FILING DATE: 15-AUG-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/086,428
 ; FILING DATE: 29 JUNE 1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/290/665
 ; FILING DATE: 15 AUGUST 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RICHARD W. BORK
 ; REGISTRATION NUMBER: 36,459
 ; REFERENCE/DOCKET NUMBER: 2026-4116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4800
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 65:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 192 amino acids
 ; STRANDEDNESS: amino acid
 ; TOPLOGY: unknown
 ; ORIGINAL SOURCE:
 ; ORGANISM: homosapiens
 ; INDIVIDUAL ISOLATE: HKS
 ; PCT-US95-10398-65

Query Match 99.5%; Score 184; DB 5; Length 192;
 Best Local Similarity 97.1%; Pred. No. 5.6e-19; Db
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 36 ; PCT-US95-10398-70
 ; Sequence 70, Application PC/TUS9510398
 ; GENERAL INFORMATION:
 ; APPLICANT: BURK, J., MILLER, R.H. AND

APPLICANT: PURCELL, R.H.
 TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
 AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
 CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
 AND THE USE OF REAGENTS DERIVED FROM THESE
 TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
 NUMBER OF SEQUENCES: 263
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/10398
 FILING DATE: 15-AUG-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/086,428
 FILING DATE: 29 JUNE 1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/290,665
 FILING DATE: 15 AUGUST 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: RICHARD W. BORK
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 751-6849
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 70:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 ORIGINAL SOURCE:
 ORGANISM: homosapiens
 INDIVIDUAL ISOLATE: S9
 PCT-US95-10398-70

Query Match 99.5%; Score 184; DB 5; Length 192;
 Best Local Similarity 97.1%; Pred. No. 5.6e-19; Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHITGHRMADMNMWNNSPTALVSQLIRI 34
 Db 116 SIYPGHVITGHRMADMNMWNNSPTALVSQLIRI 149

RESULT 37
 PCT-US95-10398-74
 Sequence 74, Application PC/TUS9510398
 ; GENERAL INFORMATION:
 ; APPLICANT: BURK, J., MILLER, R.H. AND
 ; APPLICANT: PURCELL, R.H.
 ; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
 ; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
 ; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
 ; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
 ; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
 ; NUMBER OF SEQUENCES: 263
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK

STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/10398
 FILING DATE: 15-AUG-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/086,428
 FILING DATE: 29 JUNE 1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/290,665
 FILING DATE: 15 AUGUST 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: RICHARD W. BORK
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 74:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 ORIGINAL SOURCE:
 ORGANISM: homosapiens
 INDIVIDUAL ISOLATE: T3
 PCT-US95-10398-74

Query Match 99.5%; Score 184; DB 5; Length 192;
 Best Local Similarity 97.1%; Pred. No. 5.6e-19; Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHITGHRMADMNMWNNSPTALVSQLIRI 34
 Db 116 SIYPGHVITGHRMADMNMWNNSPTALVSQLIRI 149

RESULT 38
 US-08-635-886C-190
 ; Sequence 190, Application US/08635886C
 ; Patent No. 655314
 ; GENERAL INFORMATION:
 ; APPLICANT: DELEYS, Robert
 ; APPLICANT: MERTENS, Geert
 ; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
 ; TITLE OF INVENTION: VIRUS
 ; FILE REFERENCE: 2752-18
 ; CURRENT APPLICATION NUMBER: US/08/635, 886C
 ; CURRENT FILING DATE: 1996-04-25
 ; PRIORITY APPLICATION NUMBER: PCT/EP94/03555
 ; PRIORITY FILING DATE: 1994-10-28
 ; PRIORITY APPLICATION NUMBER: EP 93402718-6
 ; PRIORITY FILING DATE: 1993-11-04
 ; NUMBER OF SEQ ID NOS: 286
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 190
 ; LENGTH: 450
 ; TYPE: PRT
 ; ORGANISM: hepatitis C virus
 US-08-635-886C-190

Query Match 99.5%; Score 184; DB 4; Length 450;
 Best Local Similarity 97.1%; Pred. No. 1.5e-18;

Search completed: November 10, 2004, 18:19:21
Job time : 39 secs

RESULT 39
US-08-635-886C-195
; Sequence 195, Application US/08635886C
; Patent No. 655114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYNS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635, 886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 195
; LENGTH: 450
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-08-635-886C-195

RESULT 40
US-08-974-690C-190
; Sequence 190, Application US/08974690C
; Patent No. 663333

; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYNS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2851-94
; CURRENT APPLICATION NUMBER: US/08/974, 690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 190
; LENGTH: 450
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-08-974-690C-190

Query Match 99.5%; Score 184; DB 4; Length 450;
Best Local Similarity 97.1%; Pred. No. 1.5e-18; Mismatches 0; Indels 0; Gaps 0;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYPGHVTGHRMADMNMWNSPTTALVVSQIRI 34
Db 307 STYPGHVTGHRMADMNMWNSPTTALVVSQIRI 340

Om protein - protein search, using sw model
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Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	185	100.0	34	US-10-414-219-23
3	185	100.0	34	US-10-665-435-15
4	185	100.0	192	US-10-128-590-87
5	185	100.0	192	US-10-128-597A-87
6	185	100.0	200	US-09-973-025-26
7	185	100.0	10	US-09-893-303-26
8	185	100.0	200	US-09-995-805-26
9	185	100.0	200	US-09-995-860-26
10	185	100.0	200	US-09-995-791-26
11	185	100.0	200	US-10-321-791-26
12	185	100.0	210	US-09-325-205-28
13	185	100.0	210	US-09-899-303-28

SUMMARIES

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17: /cgn2_6/ptodata/1/pupaa/US100_NEW_PUB.PEP:*
18: /cgn2_6/ptodata/1/pupaa/US11_NEW_PUB.PEP:*
19: /cgn2_6/ptodata/1/pupaa/US60_NEW_PUB.PEP:*
20: /cgn2_6/ptodata/1/pupaa/US60_PUBCOMB.PEP:*

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ALIGNMENTS

RESULT 2 ; US-10-414-219-23
 Sequence 23, Application US/10414219
 Publication No. US20030202987A1
 GENERAL INFORMATION:
 APPLICANT: DEPLA, ERIK
 APPLICANT: MAERTENS, GERT
 APPLICANT: BOSMAN, ALFONS
 APPLICANT: VAN WIJNENDALE, FRANS
 TITLE OF INVENTION: PARTICLES OF HCV ENVELOPE PROTEINS: USE FOR VACCINATION
 FILE REFERENCE: 135 PCT
 CURRENT APPLICATION NUMBER: US/10/414,219
 CURRENT FILING DATE: 2003-04-16
 PRIOR APPLICATION NUMBER: US/09/355,040
 PRIOR FILING DATE: 1995-07-23
 PRIOR APPLICATION NUMBER: PCT/EP99/04342
 PRIOR FILING DATE: 1999-06-23
 PRIOR APPLICATION NUMBER: EP 98870142.1
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: EP 99870033.0
 PRIOR FILING DATE: 1999-02-22
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 23
 LENGTH: 34
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-10-414-219-23

RESULT 3 ; US-10-685-435-15
 Sequence 15, Application US/10685435
 Publication No. US20040126754A1
 GENERAL INFORMATION:
 APPLICANT: Imrogenetics N.V.
 TITLE OF INVENTION: Multi-mer peptides derived from Hepatitis C Virus
 TITLE OF INVENTION: envelope proteins for diagnostic use and vaccination
 TITLE OF INVENTION: purposes.
 FILE REFERENCE: PCT98.75.HC730
 CURRENT APPLICATION NUMBER: US/10/685,435
 CURRENT FILING DATE: 2003-10-16
 PRIOR APPLICATION NUMBER: US/09/566,266B
 PRIOR FILING DATE: 2000-05-05
 PRIOR APPLICATION NUMBER: 97870179.5
 PRIOR FILING DATE: 1997-11-06
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: patenting Ver. 2.1
 SEQ ID NO: 15
 LENGTH: 34
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-10-685-435-15

RESULT 4 ; US-10-128-590-87
 Sequence 87, Application US/0128590
 Publication No. US20030108561A1
 GENERAL INFORMATION:
 APPLICANT: Imrogenetics N.V.
 TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
 FILE REFERENCE: 135 PCT
 CURRENT APPLICATION NUMBER: US/10/128,590
 CURRENT FILING DATE: 2002-07-22
 NUMBER OF SEQ ID NOS: 98
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 87
 LENGTH: 192
 TYPE: PRT
 ORGANISM: hepatitis C virus
 US-10-128-590-87

RESULT 5 ; US-10-128-587A-87
 Sequence 87, Application US/0128587A
 Publication No. US20030152940A1
 GENERAL INFORMATION:
 APPLICANT: Imrogenetics N.V.
 TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
 TITLE OF INVENTION: proteins
 FILE REFERENCE: 134 PCT
 CURRENT APPLICATION NUMBER: US/10/128,587A
 CURRENT FILING DATE: 2002-04-24
 NUMBER OF SEQ ID NOS: 98
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 87
 LENGTH: 192
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
 US-10-128-587A-87

RESULT 6 ; US-09-973-025-26
 Sequence 26, Application US/09973025
 Publication No. US20020182706A1
 GENERAL INFORMATION:
 APPLICANT: MAERTENS, GERT
 APPLICANT: BOSMAN, FONS
 APPLICANT: DE MARTINOFF, GUY
 APPLICANT: BIYSE, MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESSEES:
 ADDRESSE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA

RESULT 4

COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/973, 025
 FILING DATE: 10-OCT-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/612, 973
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32, 205
 REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-973-025-26
 Query Match 100.0%; Score 185; DB 9; Length 200;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHTGHRVADWMNNWSPTTALVSQLRI 34
 Db 166 SIYPGHTGHRVADWMNNWSPTTALVSQLRI 199
 RESULT 7
 US-09-899-303-26
 Sequence 26, Application US/09899303
 Publication No US20030036110A1
 GENERAL INFORMATION:
 APPLICANT: MAERENS, GEERT
 BOSMAN, FONS
 DE MARTINOFF, GUY
 BUYER, MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSE: NIXON & VANDERHIE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/899, 303
 FILING DATE: 06-JUL-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/612, 973
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32, 205

REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-899-303-26
 Query Match 100.0%; Score 185; DB 10; Length 200;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHTGHRVADWMNNWSPTTALVSQLRI 34
 Db 166 SIYPGHTGHRVADWMNNWSPTTALVSQLRI 199
 RESULT 8
 US-09-995-808-26
 Sequence 26, Application US/09995808
 Publication No. US20030095980A1
 GENERAL INFORMATION:
 APPLICANT: Imrogenetics N.V.
 TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.
 FILE REFERENCE: 2551-70
 CURRENT APPLICATION NUMBER: US/09/995, 808
 NUMBER OF SEQ ID NOS: 122
 SEQ ID NO 26
 LENGTH: 200
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-09-995-808-26
 Query Match 100.0%; Score 185; DB 10; Length 200;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHTGHRVADWMNNWSPTTALVSQLRI 34
 Db 166 SIYPGHTGHRVADWMNNWSPTTALVSQLRI 199
 RESULT 9
 US-09-995-860-26
 Sequence 26, Application US/09995860
 Publication No. US20030118603A1
 GENERAL INFORMATION:
 APPLICANT: Imrogenetics N.V.
 TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.
 FILE REFERENCE: 2551-69
 CURRENT APPLICATION NUMBER: US/09/995, 860
 CURRENT FILING DATE: 2001-11-29
 NUMBER OF SEQ ID NOS: 122
 SOFTWARE: PatentIn 3.1
 SEQ ID NO 26
 LENGTH: 200
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-09-995-860-26
 Query Match 100.0%; Score 185; DB 10; Length 200;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICATION NUMBER: US/09/899, 303
 FILING DATE: 06-Jul-2-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/612, 973
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32, 205
 REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 ; US-09-899-303-28
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 ; Query Match 100.0%; Score 185; DB 10; Length 210;
 ; Best Local Similarity 100.0%; Pred. No. 2.2e-18; Indels 0; Gaps 0;
 ; Matches 34; Conservative 0; Mismatches 0;
 ;
 QY 1 SIYPGHTGHRMADMNMNSPPTALVVSQIIRI 34
 Db 166 SIYPGHTGHRMADMNMNSPPTALVVSQIIRI 199
 ;
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 RESULT 14
 ; US-09-995-808-28
 ; Sequence 28, Application US/09995808
 ; Publication No. US200301095980A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
 ; FILE REFERENCE: 2551-70
 ; CURRENT APPLICATION NUMBER: US/09/995, 808
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn 3.1
 ; SEQ ID NO 28
 ; LENGTH: 210
 ; TYPE: PRT
 ; ORGANISM: Hepatitis C virus
 ;
 ; US-09-995-808-28
 ;
 ; Query Match 100.0%; Score 185; DB 10; Length 210;
 ; Best Local Similarity 100.0%; Pred. No. 2.2e-18; Indels 0; Gaps 0;
 ; Matches 34; Conservative 0; Mismatches 0;
 ;
 QY 1 SIYPGHTGHRMADMNMNSPPTALVVSQIIRI 34
 Db 166 SIYPGHTGHRMADMNMNSPPTALVVSQIIRI 199
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 ;
 RESULT 15
 ; US-09-995-860-28
 ; Sequence 28, Application US/09995860
 ; Publication No. US20030118603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
 ; FILE REFERENCE: 2551-93
 ; CURRENT APPLICATION NUMBER: US/09/995, 860
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn 3.1
 ; SEQ ID NO 28
 ; LENGTH: 210
 ; TYPE: PRT
 ; ORGANISM: Hepatitis C virus
 ;
 ; US-09-995-860-28
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 ; Query Match 100.0%; Score 185; DB 16; Length 210;
 ; Best Local Similarity 100.0%; Pred. No. 2.2e-18; Indels 0; Gaps 0;
 ; Matches 34; Conservative 0; Mismatches 0;
 ;
 QY 1 SIYPGHTGHRMADMNMNSPPTALVVSQIIRI 34
 Db 166 SIYPGHTGHRMADMNMNSPPTALVVSQIIRI 199
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RESULT 18
 US-09-973-025-4
 ; Sequence 4, Application US/09973025
 ; Publication No. US20020182706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARTENS, GEERT
 ; BOSMAN, FONS
 DE MARTYNOFF, GUY
 BYSE, MARIE-ANGE
 PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/612,973
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 1487-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 FAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 212 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-973-025-4
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 212 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-973-025-4
 Query Match 100.0%; Score 185; DB 9; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2.2e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYPGHTGHRMADMNNNSPTTAIVSQLRI 34
 Db 139 STYPGHTGHRMADMNNNSPTTAIVSQLRI 172
 RESULT 20
 US-09-995-808-4
 ; Sequence 4, Application US/09995808
 ; Publication No. US20030095980A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.
 ; FILE REFERENCE: 251-70
 ; CURRENT APPLICATION NUMBER: US/09/995,808
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn 3.1
 ; SEQ ID NO 4
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Hepatitis C virus
 ; US-09-995-808-4
 Query Match 100.0%; Score 185; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2.2e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYPGHTGHRMADMNNNSPTTAIVSQLRI 34
 Db 139 STYPGHTGHRMADMNNNSPTTAIVSQLRI 172
 RESULT 21
 US-09-995-808-4
 ; Sequence 4, Application US/09995808
 ; Publication No. US20030118603A1
 ; GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.
 TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
 TITLE OF INVENTION: therapeutic use.
 FILE REFERENCE: 2551-69
 CURRENT APPLICATION NUMBER: US/09/995, 860
 CURRENT FILING DATE: 2001-11-29
 NUMBER OF SEQ ID NOS: 122
 SOFTWARE: Patentin 3.1
 SEQ ID NO 4
 LENGTH: 212
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-09-995-860-4

Query Match 100.0%; Score 185; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2.2e-18; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SIYPGHITGHMADMNMNSPTTALVVSQRLI 34
 Db 139 SIYPGHITGHMADMNMNSPTTALVVSQRLI 172

RESULT 22
 US-09-995-791-4
 ; Sequence 4, Application US/09995791
 ; Publication No. US20030147918A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
 ; TITLE OF INVENTION: therapeutic use.
 ; FILE REFERENCE: 2551-68
 ; CURRENT APPLICATION NUMBER: US/09/995, 791
 ; CURRENT FILING DATE: 2001-11-29
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: Patentin 3.1.
 ; SEQ ID NO 4
 LENGTH: 212
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-09-995-791-4

Query Match 100.0%; Score 185; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2.2e-18; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SIYPGHITGHMADMNMNSPTTALVVSQRLI 34
 Db 139 SIYPGHITGHMADMNMNSPTTALVVSQRLI 172

RESULT 23
 US-10-321-798-4
 ; Sequence 4, Application US/10321798
 ; Publication No. US20040126395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
 ; TITLE OF INVENTION: therapeutic use.
 ; FILE REFERENCE: 2551-93
 ; CURRENT APPLICATION NUMBER: US/10/321, 798
 ; CURRENT FILING DATE: 2002-12-18
 ; CURRENT APPLICATION NUMBER: 60/418, 358
 ; PRIOR FILING DATE: 2002-10-16
 ; PRIOR APPLICATION NUMBER: 10/020, 510
 ; PRIOR FILING DATE: 2001-12-18
 ; NUMBER OF SEQ ID NOS: 123
 ; SOFTWARE: Patentin 3.1
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Hepatitis C virus
 US-10-321-798-4

Query Match 100.0%; Score 185; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2.2e-18; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SIYPGHITGHMADMNMNSPTTALVVSQRLI 34
 Db 139 SIYPGHITGHMADMNMNSPTTALVVSQRLI 172

RESULT 24
 US-09-973-025-22
 ; Sequence 22, Application US/09973025
 ; Publication No. US20020182706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MERTENS, GEERT
 ; BOSMAN, FONS
 ; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
 ; NUMBER OF SEQ ID NOS: 111
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (REPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/973, 025
 ; FILING DATE: 10-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/612,973
 ; FILING DATE: 11-MAR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BYRNE, THOMAS E.
 ; REGISTRATION NUMBER: 32, 205
 ; REFERENCE/DOCKET NUMBER: 1487-10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4000
 ; TELEFAX: (703) 816-4100
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 239 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-09-973-025-22

Query Match 100.0%; Score 185; DB 9; Length 239;
 Best Local Similarity 100.0%; Pred. No. 2.5e-18; Mismatches 0; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SIYPGHITGHMADMNMNSPTTALVVSQRLI 34
 Db 166 SIYPGHITGHMADMNMNSPTTALVVSQRLI 199

RESULT 25
 US-09-899-303-22
 ; Sequence 22, Application US/09899303
 ; Publication No. US2003003610A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MERTENS, GEERT
 ; BOSMAN, FONS

US-10-685-435-15.rabp

DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P. C.
STREET: 1100 NORTH GLIBBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,303
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-899-303-22

Query Match 100.0%; Score 185; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNMNSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNMNSPTTALVVSQRLI 199

RESULT 26

US-09-995-808-22

Sequence 22, Application US/09995808
Publication No. US20030095808A1

GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.

FILE REFERENCE: 251-70

CURRENT APPLICATION NUMBER: US/09/995,808

CURRENT FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PatentIn 3.1

SEQ ID NO: 22
LENGTH: 239
TYPE: PRT
ORGANISM: Hepatitis C virus

US-09-995-791-22

Query Match 100.0%; Score 185; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNMNSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNMNSPTTALVVSQRLI 199

RESULT 27

US-09-995-860-22

Sequence 22, Application US/09995860
Publication No. US20030118603A1

GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.

FILE REFERENCE: 251-69

CURRENT APPLICATION NUMBER: US/09/995,860

CURRENT FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PatentIn 3.1

SEQ ID NO: 22
LENGTH: 239
TYPE: PRT
ORGANISM: Hepatitis C virus

US-09-995-860-22

Query Match 100.0%; Score 185; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNMNSPTTALVVSQRLI 34
Db 166 SIYPGHTGHRMADMNMNSPTTALVVSQRLI 199

RESULT 29

US-10-321-798-22

Sequence 22, Application US/10321798
Publication No. US20040126395A1

GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.

FILE REFERENCE: 251-93

CURRENT APPLICATION NUMBER: US/10/321,798

CURRENT FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: 60/418,358

PRIOR FILING DATE: 2002-10-16

PRIOR APPLICATION NUMBER: 10/020,510
 PRIOR FILING DATE: 2001-12-18
 NUMBER OF SEQ ID NOS: 123
 SOFTWARE: PatentIn 3.1
 SEQ ID NO: 22
 LENGTH: 239
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-10-321-798-2-22

RESULT 30
 US-09-970-025-6
 Sequence 6, Application US/09970025
 GENERAL INFORMATION:
 APPLICANT: MAERTENS, GEERT
 DE MARTYNOFF, GUY
 BUYER: MARIE-ANGE
 BOSMAN, FONS
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE, P. C.
 STREET: 110 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/973,025
 FILING DATE: 10-OCT-2001
 CLASSIFICATION: <Unknown>
 PRIORITY DATA:
 APPLICATION NUMBER: US 08/612,973
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 MOLECULE TYPE: protein
 LENGTH: 263
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-999-303-6
 Query Match 100.0%; Score 185; DB 10; Length 263;
 Best Local Similarity 100.0%; Pred. No. 2.8e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYPGHTGHRMADMNNWSPTALVSQLRI 34
 Db 190 SYPGHTGHRMADMNNWSPTALVSQLRI 223

RESULT 31
 US-09-899-303-6
 Sequence 6, Application US/0999303
 Publication No. US20030036110A1
 GENERAL INFORMATION:
 APPLICANT: MARLENS, GERT
 BOSMAN, FONS
 DE MARTYNOFF, GUY
 BUYER: MARIE-ANGE
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE, P. C.
 STREET: 110 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/899,303
 FILING DATE: 06-JUL-2001
 CLASSIFICATION: <Unknown>
 PRIORITY DATA:
 APPLICATION NUMBER: US 08/612,973
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 SEQUENCE CHARACTERISTICS:
 LENGTH: 263 amino acids
 TYPE: amino acid
 TOPology: linear
 MOLECULE TYPE: protein
 LENGTH: 263
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-999-303-6
 Query Match 100.0%; Score 185; DB 10; Length 263;
 Best Local Similarity 100.0%; Pred. No. 2.8e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYPGHTGHRMADMNNWSPTALVSQLRI 34
 Db 190 SYPGHTGHRMADMNNWSPTALVSQLRI 223

RESULT 32
 US-09-995-808-6
 Sequence 6, Application US/09995808
 Publication No. US20030095980A1
 GENERAL INFORMATION:
 APPLICANT: Imagenetics N.V.
 TITLE OF INVENTION: purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.
 FILE REFERENCE: 2551-70
 CURRENT APPLICATION NUMBER: US/09/995,808
 CURRENT FILING DATE: 2001-11-29
 NUMBER OF SEQ ID NOS: 122
 SOFTWARE: PatentIn 3.1
 SEQ ID NO: 6
 LENGTH: 263

Query Match 100.0%; Score 185; DB 9; Length 263;
 Best Local Similarity 100.0%; Pred. No. 2.8e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYPGHTGHRMADMNNWSPTALVSQLRI 34
 Db 190 SYPGHTGHRMADMNNWSPTALVSQLRI 223

TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-808-6

Query Match 100.0%; Score 185; DB 10; length 263;
; Best Local Similarity 100.0%; Pred. No. 2.8e-18;
; Matches 34; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNMNSPTTALVSQLRI 34
Db 190 SIYPGHTGHRMADMNMNSPTTALVSQLRI 223

RESULT 33

; Sequence 6, Application US/09995860
; Publication No. US20030118603A1
; GENERAL INFORMATION:

; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-69
; CURRENT APPLICATION NUMBER: US/09/995, 860
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn 3.1
; SEQ ID NO 6
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-860-6

Query Match 100.0%; Score 185; DB 10; length 263;
; Best Local Similarity 100.0%; Pred. No. 2.8e-18;
; Matches 34; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNMNSPTTALVSQLRI 34
Db 190 SIYPGHTGHRMADMNMNSPTTALVSQLRI 223

RESULT 34

; Sequence 6, Application US/09995791
; Publication No. US20030147918A1
; GENERAL INFORMATION:

; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-68
; CURRENT APPLICATION NUMBER: US/09/995, 791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn 3.1
; SEQ ID NO 6
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-791-6

Query Match 100.0%; Score 185; DB 10; length 263;
; Best Local Similarity 100.0%; Pred. No. 2.8e-18;
; Matches 34; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNMNSPTTALVSQLRI 34
Db 190 SIYPGHTGHRMADMNMNSPTTALVSQLRI 223

RESULT 35

; Sequence 6, Application US/09995798
; Publication No. US2003018603A1
; GENERAL INFORMATION:

; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-93
; CURRENT APPLICATION NUMBER: US/10/321, 798
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/418, 358
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 10/020, 510
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn 3.1
; SEQ ID NO 6
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-10-321-798-6

Query Match 100.0%; Score 185; DB 16; length 263;
; Best Local Similarity 100.0%; Pred. No. 2.8e-18;
; Matches 34; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNMNSPTTALVSQLRI 34
Db 190 SIYPGHTGHRMADMNMNSPTTALVSQLRI 223

RESULT 36

; Sequence 48, Application US/09973025
; Publication No. US20030182706A1
; GENERAL INFORMATION:

; APPLICANT: MAERIENS, GEERT
; BOSMAN, FONS
; DE MARTINOFF, GUY
; BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/973, 025
; FILING DATE: 10-OCT-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/612, 973
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 692
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 48;

RESULT 35

; Sequence 6, Application US/10321798-6
; Publication No. US2003018603A1
; Sequence 6, Application US/09995860
; Publication No. US20030118603A1

US-09-973-025-48

Query Match: 100.0%; Score 185; DB 9; Length 692;
 Best Local Similarity 100.0%; Pred. No. 8.1e-18;
 Matches 34; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNNTSPTAIWSQLRI 34
 Db 190 SIYPGHTGHRMADMNNTSPTAIWSQLRI 223

RESULT 37

US-09-899-303-48

Sequence 48, Application US/09899303
 Publication No. US20030103610A1

GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT

BOSMAN, FONS

DE MARTYNOFF, GUY

BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS: ADDRESSEE: NIXON & VANDERHYPE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/899,303

FILING DATE: 06-JUL-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/612,973

FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4400

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 692 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 48:

US-09-899-303-48

Query Match: 100.0%; Score 185; DB 10; Length 692;
 Best Local Similarity 100.0%; Pred. No. 8.1e-18;
 Matches 34; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNNTSPTAIWSQLRI 34
 Db 190 SIYPGHTGHRMADMNNTSPTAIWSQLRI 223

RESULT 38

US -09-955-808-48
 Sequence 48, Application US/09995808
 Publication No. US20030095980A1

GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.

FILE REFERENCE: 2551-70

CURRENT APPLICATION NUMBER: US/09/995, 808

CURRENT FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PatentIn 3.1

SEQ ID NO 48

LENGTH: 692

TYPE: PRT

ORGANISM: Hepatitis C virus

US-09-995-808-48

Query Match: 100.0%; Score 185; DB 10; Length 692;
 Best Local Similarity 100.0%; Pred. No. 8.1e-18;
 Matches 34; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNNTSPTAIWSQLRI 34
 Db 190 SIYPGHTGHRMADMNNTSPTAIWSQLRI 223

RESULT 39

US-09-995-860-48
 Sequence 48, Application US/09995860
 Publication No. US20030118603A1

GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.

FILE REFERENCE: 2551-69

CURRENT APPLICATION NUMBER: US/09/995, 860

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PatentIn 3.1

SEQ ID NO 48

LENGTH: 692

TYPE: PRT

ORGANISM: Hepatitis C virus

US-09-995-860-48

Query Match: 100.0%; Score 185; DB 10; Length 692;
 Best Local Similarity 100.0%; Pred. No. 8.1e-18;
 Matches 34; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 SIYPGHTGHRMADMNNTSPTAIWSQLRI 34
 Db 190 SIYPGHTGHRMADMNNTSPTAIWSQLRI 223

RESULT 40

US-09-995-791-48
 Sequence 48, Application US/09995791
 Publication No. US20030147918A1

GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.

FILE REFERENCE: 2551-68

CURRENT APPLICATION NUMBER: US/09/995, 791

CURRENT FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PatentIn 3.1

SEQ ID NO 48

LENGTH: 692

TYPE: PRT

ORGANISM: Hepatitis C virus

US-09-995-791-48

Query Match: 100.0%; Score 185; DB 10; Length 692;
 Best Local Similarity 100.0%; Pred. No. 8.1e-18;
 Matches 34; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY	1	SIYPGHTGHRNAWDMMMWSSPTTALVWSQQLRI	34
Db	190	SIYPGHTGHRNAWDMMMWSSPTTALVWSQQLRI	223

Search completed: November 10, 2004, 18:30:03
Job time : 141 secs

Copyright GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2004, 18:09:09 ; Search time 37 Seconds
(without alignments)
83.415 Million cell updates/sec

Title: US-10-685-435-15
Perfect score: 185
Sequence: 1 SIYPGHTGHRMADMNNWSPTALVSQLRI 34

Scoring table: BL05M62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	99.5	177	2	SI52123 genome polyprotein
2	184	99.5	177	2	S33743 genome polyprotein
3	184	99.5	550	2	JH0711 genome polyprotein
4	184	99.5	3010	1	GIWVTC genome polyprotein
5	183	98.9	177	2	S22745 genome polyprotein
6	182	98.4	177	2	S32749 genome polyprotein
7	181	97.8	177	2	S22746 genome polyprotein
8	181	97.8	640	2	JQ1584 genome polyprotein
9	180	97.3	177	2	S33741 genome polyprotein
10	180	97.3	315	2	PN0011 envelope glycoprotein
11	180	97.3	787	2	PN0677 hypothetical protein
12	180	97.3	3010	1	A45573 genome polyprotein
13	180	97.3	973	1	GIWVTC genome polyprotein
14	180	97.3	3010	1	GIWVTC genome polyprotein
15	179	96.8	322	2	JN0265 genome polyprotein
16	179	96.8	513	2	PC1284 genome polyprotein
17	179	96.8	3011	1	GIWVTC genome polyprotein
18	178	96.2	315	2	PS0164 envelope glycoprotein
19	178	96.2	782	2	SL08032 genome polyprotein
20	178	96.2	3010	1	SL08030 genome polyprotein
21	177	95.7	513	2	A44150 structural protein
22	176	95.1	369	2	S21471 genome polyprotein
23	175	94.6	441	2	S22707 genome polyprotein
24	175	94.6	520	2	JQ1925 polyprotein - hepa
25	174	94.1	782	2	SL08035 genome polyprotein
26	174	94.1	3011	1	S40770 genome polyprotein
27	173	93.5	315	2	PS0165 envelope glycoprotein
28	173	93.5	415	2	PC4407 envelope protein - polypeptide
29	173	93.5	523	2	JQ1926

ALIGNMENTS

RESULT 1
S25123 genome polyprotein (clone Glob.1) - hepatitis C virus (fragment)
N;Contains: envelope protein El
C;Species: hepatitis C virus
C;Date: 20-Feb-1995 #sequence_revision 26-Jul-1995 #text_change 09-Jul-2004
C;Accession: S25123
R;Hoehne, M.; Schreier, B.; Fuchs, K.; Wise, M.; Deinhardt, F.; Roggendorf, M.
submitted to the EMBL Data Library, April 1992
A;Description: Variability of E 1 gene region of Hepatitis C virus in patients infected
A;Reference number: S25123
A;Accession: S25123
A;Molecule type: genomic RNA
A;Residues: i-177 <HOE>
A;Cross-references: UNIPROT:Q68909; EMBL:Y67299; NID:959470; PID:CAA47713.1; PID:959471
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: envelope protein; polyprotein
F;1-177/Product: envelope protein El #status predicted <WAT>

Query Match 99.5%; Score 144; DB 2; Length 177;
Best Local Similarity 97.1%; Pred. No. 1.4e-18; 0; Mismatches 33; Conservative 1; Indels 0; Gaps 0;

Qy 1 SIYPGHTGHRMADMNNWSPTALVSQLRI 34
Db 111 SIYPGHTGHRMADMNNWSPTALVSQLRI 144

RESULT 2
S22743 genome polyprotein - hepatitis C virus (isolate EG-1) (fragment)
N;Contains: envelope protein El
C;Species: hepatitis C virus
A;Variety: isolate EG-1
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S32743
R;Roggendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, B.
submitted to the EMBL Data Library, February 1993
A;Description: Variability of the envelope regions of HCV in European isolates and its
A;Reference number: S32741
A;Molecule type: genomic RNA
A;Residues: i-177 <ROG>
A;Cross-references: UNIPROT:Q06618; EMBL:X72980; NID:9296104; PID:CAA51485.1; PID:92961
A;Experimental source: isolate EG-1
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: envelope protein; polyprotein
F;1-177/Product: envelope protein El #status predicted <WAT>

Query Match 99.5%; Score 144; DB 2; Length 177;
Best Local Similarity 97.1%; Pred. No. 1.4e-18; 0; Mismatches 33; Conservative 1; Indels 0; Gaps 0;

Query Match 99.5%; Score 184; DB 1; Length 3010;
 N; Contains: envelope protein E1;保守性 97.1%; Prod. No. 3; 4e-17;
 C; Species: hepatitis C virus
 N; Contains: envelope protein E1
 C; Accession: JH0711 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 R; Liu, K.; Hu, Z.; Li, H.; Prince, A.M.; Inchauspe, G.
 Gene 114, 245-250, 1992
 A; Title: Genomic typing of hepatitis C viruses present in China.
 A; Reference number: JH0711; MUID:92290283; PMID:1318245
 A; Accession: JH0711
 A; Molecule type: genomic RNA
 A; Residues: 1-550 <LINS>
 A; Cross-references: UNIPROT:Q7L2W4; GB:W7488; GB:W74889
 A; Note: translation of the nucleotide sequence is not complete
 C; Superfamily: hepatitis C virus genome polyprotein
 C; Keywords: envelope protein; glycoprotein; nonstructural protein; nucleocapsid; polyprotein
 F; 1-190/Product: envelope protein C #status predicted <EGC>
 F; 191-360/Product: nucleocapsid protein B1 #status predicted <EGC>
 F; 361-550/Product: envelope protein B2 or nonstructural protein NS5 (fragment) #status predicted <NS5>
 F; 515-550/Product: nonstructural protein NS5 (fragment) #status predicted <NS5>
 F; 196, 233, 250, 305, 416, 422, 429, 447/Binding site: carbohydrate (Asn) (covalent) #status predicted <NS5>
 Query Match 99.5%; Score 184; DB 2;
 Best Local Similarity 97.1%; Pred. No. 5; 1e-18;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYGHITGHRMADMNNWSPTALVSQLRI 34
 Db 307 SIYGHITGHRMADMNNWSPTALVSQLRI 340

RESULT 4
 GNNWTV
 genome polyprotein - hepatitis C virus (strain Taiwan)
 N; Contains: capsid protein C; envelope protein M; hepacivirus (EC 3.4.21.98) (nonstructural protein NS4a); nonstructural protein NS4b; nonstructural protein NS5
 C; Species: hepatitis C virus
 A; Note: host Homo sapiens (man)
 C; Accession: A40244 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 R; Chen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S.
 Virology 188, 102-113, 1992
 A; Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the
 A; Reference number: A40244; MUID:92230206; PMID:1314449
 A; Accession: A40244
 A; Molecule type: genomic RNA
 A; Residues: 1-3010 <CPR>
 A; Cross-references: UNIPROT:P29846; GB:W64754
 A; Molecule type: genomic RNA
 A; Residues: 1-3010 <CPR>
 C; Superfamily: hepatitis C virus genome polyprotein
 C; Keywords: AMP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 F; 1-115/Product: capsid protein C #status predicted <CPR>
 F; 116-191/Product: envelope protein M #status predicted <CPR>
 F; 192-389/Product: major envelope protein C #status predicted <MEB>
 F; 390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F; 730-1066/Product: nonstructural protein NS2 #status predicted <NS2>
 F; 1007-1615/Product: hepacivirus #status predicted <NS3>
 F; 1220-1277/Region: nucleotide binding motif A (P-loop)
 F; 1312-1317/Region: nucleotide binding motif B
 F; 1316-1319/Region: DXH motif
 F; 1615-1862/Product: nonstructural protein NS4a #status predicted <NS4a>
 F; 8863-2013/Product: nonstructural protein NS5 #status predicted <NS5>
 F; 196, 209, 233, 234, 250, 305, 325, 417, 423, 430, 448, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 207

Query Match 99.5%; Score 184; DB 1; Length 3010;
 N; Contains: envelope protein E1;保守性 97.1%; Prod. No. 3; 4e-17;
 C; Species: hepatitis C virus
 N; Contains: envelope protein E1
 C; Accession: S32745 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 R; Roggendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, E.
 submitted to the EMBL Data Library, February 1993
 A; Description: Variability of the envelope regions of HCV in European isolates and its significance
 A; Reference number: S32741
 A; Molecule type: genomic RNA
 A; Residues: 1-177 <RGS>
 A; Cross-references: UNIPROT:Q06619; EMBL:X72982; MUID:9296108; PIDN:CAAS1487.1; PID:92961
 C; Superfamily: hepatitis C virus genome polyprotein
 C; Keywords: envelope protein; polyprotein
 F; 1-177/Product: envelope protein E1 #status predicted <MAT>
 Query Match 98.9%; Score 183; DB 2;
 Best Local Similarity 97.1%; Pred. No. 2e-18;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYGHITGHRMADMNNWSPTALVSQLRI 34
 Db 111 SIYGHITGHRMADMNNWSPTALVSQLRI 144

RESULT 5
 S32745
 genome polyprotein - hepatitis C virus (isolate EG-2) (fragment)
 N; Contains: envelope protein E1
 C; Species: hepatitis C virus
 A; Variety: isolate EG-2
 C; Accession: S32745
 C; Superfamily: hepatitis C virus genome polyprotein
 C; Keywords: envelope protein; polyprotein
 F; 1-177/Product: envelope protein E1 #status predicted <MAT>
 Query Match 98.9%; Score 183; DB 2;
 Best Local Similarity 97.1%; Pred. No. 2e-18;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYGHITGHRMADMNNWSPTALVSQLRI 34
 Db 111 SIYGHITGHRMADMNNWSPTALVSQLRI 144

RESULT 6
 S32749
 genome polyprotein - hepatitis C virus (isolate RU-1) (fragment)
 N; Contains: envelope protein E1
 C; Species: hepatitis C virus
 A; Variety: isolate RU-1
 C; Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C; Accession: S32749
 R; Roggendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, E.
 submitted to the EMBL Data Library, February 1993
 A; Description: Variability of the envelope regions of HCV in European isolates and its significance
 A; Reference number: S32741
 A; Accession: S32749
 A; Molecule type: genomic RNA
 A; Residues: 1-177 <RGS>
 A; Cross-references: UNIPROT:Q06613; EMBL:X72975; MUID:9296114; PIDN:CAAS1480.1; PID:92961
 C; Superfamily: hepatitis C virus genome polyprotein
 C; Keywords: envelope protein; polyprotein
 F; 1-177/Product: envelope protein E1 #status predicted <MAT>
 Query Match 98.4%; Score 182; DB 2;
 Best Local Similarity 94.1%; Pred. No. 2; 8e-18;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYGHITGHRMADMNNWSPTALVSQLRI 34
 Db 111 SIYGHITGHRMADMNNWSPTALVSQLRI 144

RESULT 7
 S32746
 genome polyprotein - hepatitis C virus (isolate HU-1) (fragment)
 N; Contains: envelope protein E1

C;Species: hepatitis C virus
 A;Variety: isolate HU-1
 C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C;Accession: S32746
 R;Roggendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, E.
 submitted to the EMBL Data Library, February 1993
 A;Description: Variability of the envelope regions of HCV in European isolates and its s
 A;Accession: S32746
 A;Residues: 1-177 <ROG>
 A;Cross-references: UNIPROT:Q06612; EMBL:X72976; NID:9296110; PIDN:CAA51481.1; PID:92961
 A;Experimental source: Isolate HU-1
 A;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: envelope protein; polyprotein
 F;1-177/Product: envelope protein El #status predicted <MAT>
 Query Match 97.8%; Score 181; DB 2; Length 177;
 Best Local Similarity 97.1%; Pred. No. 3.8e-18;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 A;Accession: JQ01584
 Qy 1 SIYPGHTGHRMADMNNNSPTALVSQLRI 34
 Db 111 SIYPGHISGHRAWDMMNNNSPTALVSQLRI 144

RESULT 8
 JQ01584
 genome polyprotein - hepatitis C virus (strain U.K.) (fragment)
 N;Contains: core protein C; envelope protein E2; nonstructural prot
 C;Species: hepatitis C virus
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C;Accession: JQ01584
 R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992
 A;Title: Cloning and sequencing of the structural region and expression of putative core
 A;Reference number: JQ01584; MUID:92300349; PMID:1318944
 A;Accession: JQ01584
 A;Molecule type: genomic RNA
 A;Residues: 1-640 <KUM>
 A;Cross-references: UNIPROT:Q68366; GB:X84079; NID:9643119; PIDN:CAA58808.1; PID:9643120
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: core protein C; envelope protein; glycoprotein; nonstructural protein; polypro
 F;1-191/Product: core protein C #status predicted <GPC>
 F;1-191-380/Product: envelope protein El #status predicted <EE1>
 F;1-390-640/Product: envelope protein E2 and nonstructural protein; polypro
 F;1-196, 209, 234, 305, 417, 430, 448, 476, 540, 556, 576, 623/Binding site: carbohydrate (Asn) (covalent)
 Query Match 97.8%; Score 181; DB 2; Length 640;
 Best Local Similarity 94.1%; Pred. No. 1.6e-17;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 A;Accession: QY111
 Qy 1 SIYPGHTGHRMADMNNNSPTALVSQLRI 34
 Db 307 SIYPGHISGHRAWDMMNNNSPTALVSQLRI 340

RESULT 9
 S32741
 genome polyprotein - hepatitis C virus (isolate CR-1) (fragment)
 N;Contains: envelope protein El
 C;Species: hepatitis C virus
 A;Variety: isolate CR-1
 C;Date: 06-Jun-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C;Accession: S32741
 R;Roggendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, E.
 submitted to the EMBL Data Library, February 1993
 A;Description: Variability of the envelope regions of HCV in European isolates and its s
 A;Accession: S32741
 A;Residues: 1-177
 A;Cross-references: UNIPROT:Q06617; EMBL:X72978; NID:9296100; PIDN:CAA51483.1; PID:92961

A;Experimental source: isolate CR-1
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: envelope protein El #status predicted <MAT>
 F;1-177/Product: envelope protein El #status predicted <MAT>
 Query Match 97.3%; Score 180; DB 2; Length 787;
 Best Local Similarity 94.1%; Pred. No. 2.8e-17;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 A;Accession: QY111
 Qy 1 SIYPGHTGHRMADMNNNSPTALVSQLRI 34
 Db 307 SIYPGHISGHRAWDMMNNNSPTALVSQLRI 340

RESULT 10
 PN0011
 envelope glycoprotein (clone 63) - hepatitis C virus (fragment)
 C;Species: hepatitis C virus
 C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
 C;Accession: PN0011
 R;Hijikata, M.; Kato, N.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Shimotohno, K.
 Biochem. Biophys. Res. Commun. 175, 222-228, 1991
 A;Title: Hypervariable regions in the putative glycoprotein of hepatitis C virus.
 A;Reference number: PN0011; MUID:9151353; PMID:1647805
 A;Accession: PN0011
 A;Molecule type: genomic RNA
 A;Residues: 1-315 <Hij>
 A;Cross-references: UNIPROT:Q00904; GB:DD00689
 A;Note: the authors translated the codon GAC for residue 27 as Gln and GAT for residue 1.
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: glycoprotein; polyprotein
 F;200-209/Region: hypervariable 2 #status predicted
 F;283-289/Region: hypervariable 2 #status predicted
 F;5,18,43,59,114,134,226,232,239,257/Binding site: carbohydrate (Asn) (covalent) #status
 Query Match 97.3%; Score 180; DB 2; Length 315;
 Best Local Similarity 94.1%; Pred. No. 1e-17;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 A;Accession: QY116
 Qy 1 SIYPGHTGHRMADMNNNSPTALVSQLRI 34
 Db 116 SIYPGHISGHRAWDMMNNNSPTALVSQLRI 149

RESULT 11
 PN0677
 hypothetical protein 787 - hepatitis C virus (fragment)
 C;Species: hepatitis C virus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
 C;Accession: PN0677
 R;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
 Biochem. Biophys. Res. Commun. 196, 780-788, 1993
 A;Title: Genomic typing of hepatitis C viruses from Korean Patients: Implications of gen
 A;Reference number: PN0677; MUID:94059104; PMID:8240354
 A;Accession: PN0677
 A;Molecule type: mRNA
 A;Residues: 1-787 <CHO>
 A;Cross-references: UNIPROT:Q08244; GB:II20498; NID:91381031; PIDN:AA02608.1; PID:913810
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: glycoprotein; nonstructural protein
 F;196-209, 234-250, 305, 325, 421, 427, 452, 536, 544, 560, 580, 627, 649/Binding site: carbohydrate
 Query Match 97.3%; Score 180; DB 2; Length 787;
 Best Local Similarity 94.1%; Pred. No. 2.8e-17;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

genome polyprotein - hepatitis C virus (strain JY) #status predicted <JY>
 N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructural protein NS4a); nonstructural protein NS4b; nonstructural protein NS5
 C;Species: hepatitis C virus
 C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
 C;Accession: A45573
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-310 <TA>
 A;Cross-references: UNIPROT:Q00269; GB:D11168; GB:D01171; NID:9221612; PIDN:BAA01943.1;
 A;Experimental source: HCV-JT
 A;Note: sequence extracted from NCBI backbone (NCBIN:106206, NCBIPI:106207)
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
 P;2-115/Product: capsid protein C #status predicted <CPC>
 P;116-191/Product: envelope protein M #status predicted <EPM>
 F;119-389/Product: major envelope protein E #status predicted <MEE>
 F;1390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 P;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 P;1007-1615/Product: hepacivirin #status predicted <NS3>
 P;1230-1235/Region: nucleotide-binding motif A (P-loop)
 P;1312-1317/Region: nucleotide-binding motif B
 F;1316-1319/Region: DEXH motif
 P;1863-2013/Product: nonstructural protein NS4a #status predicted <NS4>
 P;2014-3010/Product: nonstructural protein NS4b #status predicted <NS5>
 Query Match: Best Local Similarity 97.3%; Score 180; DB 1; Length 3010;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qv. 1 STYPRGHITGHRMAMDDMMNNWNSPTAIVSQRRI 34
 Db 307 SIYPGVSVSGRHMRMAMDDMMNNWNSPTAIVSQRRI 340

RESULT 13
 GWNCJ
 Genome polyprotein - hepatitis C virus (strain J)
 N;Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C;Species: hepatitis C virus
 C;Accession: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C;Accession: A32523; PS0056
 R;Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimotohno, K.; Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990
 A;Title: Molecular cloning of the human hepatitis C virus genome from Japanese patients
 A;Reference number: A39253; MUID:9108850; PMID:2175903
 A;Accession: A32523
 A;Molecule type: generic RNA
 A;Residues: 1-3010 <KAT>
 A;Cross-references: UNIPROT:P66622; GB:D90206; NID:9221610; PIDN:BAA14233.1; PID:9221611
 R;Kato, N.; Ohkoshi, S.; Shimotohno, K.
 Proc. Jpn. Acad. 65B, 219-223, 1989
 A;Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence variation
 A;Reference number: PS0085
 A;Accession: PS0086
 A;Molecule type: generic RNA
 A;Residues: 2650-2707 <KA2>
 A;Experimental source: Japanese isolate
 C;Comment: The cleavage sites of this polyprotein have not been determined.
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
 P;2-115/Product: capsid protein C #status predicted <CPC>
 F;116-191/Product: envelope protein M #status predicted <EPM>
 F;119-389/Product: major envelope protein E #status predicted <MEE>
 F;1390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F;1316-1006/Product: nonstructural protein NS2 #status predicted <NS2>

A;Residues: 1-322 <P0C>	A;Molecule type: genomic RNA
A;Cross-references: UNIPROT:Q03729; GB:W61717; GB:M61718	A;Residues: 157-1633 <CH2>
A;Note: the authors translated the codon GCA for residue 198 as Tyr	A;Experimental source: isolates E-b17
C;Superfamily: hepatitis C virus genome polyprotein	C;Species: hepatitis C virus
C;Keywords: capsid protein; envelope protein; glycoprotein; polyprotein; transmembrane protein	C;Variety: isolate JK4
F;1-109/Product: capsid protein C (fragment) #status predicted <COR>	C;Accession: S1032
F;110-178/Product: envelope protein M (fragment) #status predicted <PM>	R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
F;163-178/Domain: transmembrane #status predicted <TM1>	Submitted to the EMBL Data Library, September 1991
F;179-322/Product: major envelope protein B (fragment) #status predicted <ENV>	A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus is currently in progress.
F;253-269/Domain: transmembrane #status predicted <TM2>	A;Reference number: S18029
F;191,216/Binding site: carbohydrate (Asn) (covalent) #status predicted	A;Accession: S18032
Query Match 96.8%; Score 179; DB 2; Length 322;	A;Molecule type: genomic RNA
Best Local Similarity 94.1%; Pred. No. 1.4e-17;	A;Residues: 1-782 <HN>
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 SIYPGHTCHRMAWDMMNNWSPTALVSQLRI 34	
Db 289 SIYPGHTCHRMAWDMMNNWSPTALVSQLRI 322	
RESULT 16	
PC1284 genome polyprotein - hepatitis C virus (isolate HC-J4) (fragment)	
C;Species: hepatitis C virus	
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004	
C;Accession: PC1284	
A;Molecule type: genomic RNA	
A;Residues: 1-153 <OKA>	
A;Cross-references: UNIPROT:Q81221; GB:D00832; NID:9221513; PIDN:BA00705.1; PID:9221514	
C;Superfamily: hepatitis C virus genome polyprotein	
Query Match 96.8%; Score 179; DB 2; Length 513;	
Best Local Similarity 94.1%; Pred. No. 2.4e-17;	
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 SIYPGHTCHRMAWDMMNNWSPTALVSQLRI 34	
Db 307 SIYPGHTCHRMAWDMMNNWSPTALVSQLRI 340	
RESULT 17	
GNWV3 genome polyprotein - hepatitis C virus (strain HCV-1)	
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5)	
C;Species: hepatitis C virus	
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004	
C;Accession: A39166; PQ0403; PQ0404	
R;Choc, O.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C.; Coli, Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991	
A;Title: Genetic organization and diversity of the hepatitis C virus.	
A;Reference number: A39166; MUID:91172826; PMID:1848704	
A;Accession: A39166	
A;Molecule type: mRNA	
A;Cross-references: UNIPROT:P26664; GB:W62321; NID:9329873; PIDN:AAA45676.1; PID:9329874	
R;Chan, S.W.; McCormish, F.; Holmes, E.C.; Dow, B.; Peutherford, J.F.; Follett, E.; Yap, P.I.; Gen. Virol. 73, 1131-1141, 1992	
A;Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to e	
A;Accession: PQ0403	
A;Molecule type: genomic RNA	
A;Residues: 157-1633 <CHA>	
A;Cross-references: DDBJ:D01028	
A;Experimental source: isolates E-b16	
A;Accession: PQ0404	
A;Status: preliminary	
RESULT 18	
PS0164 envelope glycoprotein (clone 64) - hepatitis C virus (fragment)	
C;Species: hepatitis C virus	
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004	
C;Accession: PS0164	
R;Hijikata, M.; Kato, N.; Ootsuyama, Y.; Nakadawa, M.; Ohkoshi, S.; Shimotohno, K. Biochem. Biophys. Res. Commun. 175, 220-228, 1991	
A;Title: Hypervariable regions in the putative glycoprotein of hepatitis C virus.	
A;Reference number: P0011; MUID:91151353; PMID:1847805	
A;Accession: PS0164	
A;Molecule type: genomic RNA	
A;Residues: 1-315 <HN>	
A;Cross-references: UNIPROT:Q00905; GB:D00690	
A;Note: the authors translated the codon GAC for residues 27 and 112 as Glu	
C;Superfamily: hepatitis C virus genome polyprotein	
F;200-209/Region: hypervariable I #status predicted	
F;283-289/Region: hypervariable I #status predicted	
F;5,18,43,59,114,134-226,232,239,257,287/Binding site: carbohydrate (Asn) (covalent)	
Query Match 96.2%; Score 178; DB 2; Length 315;	
Best Local Similarity 94.1%; Pred. No. 1.9e-17;	
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy 1 SIYPGHTCHRMAWDMMNNWSPTALVSQLRI 34	
Db 116 SIYPGHTCHRMAWDMMNNWSPTALVSQLRI 149	
RESULT 19	
S18032 genome polyprotein - hepatitis C virus (isolate JK4) (fragment)	
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/EE2 protein	
C;Species: hepatitis C virus	
C;Variety: isolate JK4	
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004	
C;Accession: S1032	
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.	
Submitted to the EMBL Data Library, September 1991	
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus is currently in progress.	
A;Reference number: S18029	
A;Accession: S18032	
A;Molecule type: genomic RNA	
A;Residues: 1-782 <HN>	

QY 1 SIYPGHITGHRMADMNNWSPTTALVSQLRI 34
 Db 307 SIYPGHVSGHRMADMNNWSPTAALVSQLRI 340

RESULT 24
 JQ1925
 Polyprotein - hepatitis C virus (isolate HCV-KF)
 N;Contains: C protein; E1 protein; E2/NS1 protein
 C;Species: hepatitis C virus
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 C;Accession: JQ1925
 R;Abe, K.; Inchauspe, G.; Fujisawa, K.
 J. Gen. Virol. 73, 2125-2129, 1992
 A;Title: Genomic characterization and mutation rate of hepatitis C virus isolated from a
 A;Reference number: JQ1925; MUID:93019030; PMID:1383400
 A;Accession: JQ1925
 A;Molecule type: mRNA
 A;Residues: 1-1520 <AER>
 A;Cross-references: UNIPROT:Q01403; DBPI:DI10687; NID:9221544; PIDN:BA01529.1; PID:92215
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: polyprotein; transmembrane protein
 F1-91/Product: C protein #status predicted <CPR>
 F1-92-383/Product: E1 protein #status predicted <E1R>
 F384-520/Product: E2/NS1 protein #status predicted <E2P>

Query Match 94.6%; Score 175; DB 2; Length 520;
 Best Local Similarity 91.2%; Pred. No. 8.9e-17; Mismatches 31; Indels 0; Gaps 0;
 Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMADMNNWSPTTALVSQLRI 34
 Db 307 SIYPGHVSGHRMADMNNWSPTAALVSQLRI 340

RESULT 25
 S19875

Query Match 94.6%; Score 175; DB 2; Length 520;
 Best Local Similarity 91.2%; Pred. No. 8.9e-17; Mismatches 31; Indels 0; Gaps 0;
 Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
 C;Species: hepatitis C virus
 A;Variety: isolate JK3
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C;Accession: S19875
 R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
 submitted to the EMBL Data Library, September 1991
 A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso-
 A;Reference number: S18029
 A;Accession: S19875
 A;Molecule type: genomic RNA
 A;Residues: 1-182 <HIN>
 A;Cross-references: UNIPROT:Q08951; EMBL:X61592; NID:959482; PIDN:CA43789.1; PID:959483
 A;Experimental source: isolate JK3
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
 F1-191/Product: core protein #status predicted <MAT1>
 F1-192-383/Product: envelope protein 1 #status predicted <MAT2>
 F384-733/Product: NS1/E2 protein #status predicted <MAT3>
 F384-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 94.1%; Score 174; DB 2; Length 782;
 Best Local Similarity 94.1%; Pred. No. 2e-16; Mismatches 32; Conservative 1; Indels 0; Gaps 0;
 Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMADMNNWSPTTALVSQLRI 34
 Db 307 SIYPGHVSGHRMADMNNWSPTAALVSQLRI 340

RESULT 26
 S40770

Query Match 94.1%; Score 174; DB 2; Length 782;
 Best Local Similarity 94.1%; Pred. No. 2e-16; Mismatches 32; Conservative 1; Indels 0; Gaps 0;
 Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMADMNNWSPTTALVSQLRI 34
 Db 307 SIYPGHVSGHRMADMNNWSPTAALVSQLRI 340

RESULT 26
 S40770
 genome polyprotein - hepatitis C virus
 N;Contains: capsid protein C; envelope protein M; hepacivirus (EC 3.4.21.98) (nonstructu-

protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C;Species: hepatitis C virus
 C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
 C;Accession: S40770; PCI285
 R;Okamoto, H.
 submitted to the EMBL Data Library, March 1992
 A;Reference number: S40770
 A;Accession: S40770
 A;Molecule type: genomic RNA
 A;Residues: 1-3011 <OKA>
 A;Cross-references: UNIPROT:Q03463; EMBL:D10749; NID:9221586; PIDN:BA01582.1; PID:92215
 R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, Jpn. J. Exp. Med. 60, 167-177, 1990
 A;Title: The 5'-terminal sequence of the hepatitis C virus genome.
 A;Reference number: PC1284; MUID:9101316; PMID:210712
 A;Accession: PC1285
 A;Molecule type: genomic RNA
 A;Residues: 1-513 <OK2>
 A;Experimental source: isolate HC-J1
 C;Superfamily: hepatitis C Virus genome polyprotein
 C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
 F2-115/Product: capsid protein C #status predicted <CPC>
 F1-16-191/Product: envelope protein M #status predicted <EPM>
 F1-192-389/Product: major envelope protein E #status predicted <MEB>
 F390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F1230-1237/Region: nucleotide-binding motif A (P-loop)
 F1312-1317/Region: nucleotide-binding motif B
 F1316-1319/Region: DEXH motif
 F1863-2013/Product: nonstructural protein NS3 #status predicted <NS3>
 F2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match 94.1%; Score 174; DB 1; Length 3011;
 Best Local Similarity 91.2%; Pred. No. 8.9e-16; Mismatches 31; Indels 0; Gaps 0;
 Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMADMNNWSPTTALVSQLRI 34
 Db 307 SIYPGHVSGHRMADMNNWSPTAALVSQLRI 340

RESULT 27
 PS0165
 envelope glycoprotein (clone 168) - hepatitis C virus (fragment)
 C;Species: hepatitis C virus
 C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
 C;Accession: PS0165
 R;Hijikata, M.; Kato, N.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Shimotohno, K.
 Biochem. Biophys. Res. Commun. 175, 220-228, 1991
 A;Title: Hypervariable regions in the putative glycoprotein of hepatitis C virus.
 A;Reference number: P0011; MUID:9115135; PMID:1847805
 A;Accession: PS0165
 A;Molecule type: genomic RNA
 A;Residues: 1-315 <HI2>
 A;Cross-references: UNIPROT:Q00056; GB:DB0691
 A;Note: the authors translated the codon GAC for residues 27 and 112 as Glu and CTR for
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: glycoprotein; polyprotein
 F200-209/Region: hypervariable 1 #status predicted
 F283-289/Region: hypervariable 2 #status predicted
 F5,18,59,114,134,226,232,239,257/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 93.5%; Score 173; DB 2; Length 315;
 Best Local Similarity 88.2%; Pred. No. 9.8e-17; Mismatches 30; Indels 0; Gaps 0;
 Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMADMNNWSPTTALVSQLRI 34
 Db 116 SIYPGHVSGHRMADMNNWSPTAALVSQLRI 149

RESULT 28
 envelope protein - hepatitis C virus (fragment)
 C;Species: hepatitis C virus
 C;ID: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
 C;Accession: PC4407
 R;Li, G.; Yeo, J.; Peng, W.
 Chinese J. Virol. 13, 24-32, 1997
 A;Title: Sequence of genomic region of hepatitis C virus envelope proteins from a Giang
 A;Reference number: PC4407
 A;Accession: PC4407
 A;Molecule type: genomic RNA
 A;Cross-references: UNIPROT:Q17ZY4
 A;Note: the authors translated the codon ATA for residues 93 and 249 as Met
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: envelope protein

RESULT 29
 Query Match 93.5%; Score 173; DB 2; Length 415;
 Best Local Similarity 88.2%; Pred. No. 1.3e-16; Mismatches 1; Indels 0; Gaps 0;
 Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 C;Species: hepatitis C virus
 C;Accession: 03-MAY-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
 C;Accession: JQ1926
 R;Abe, K.; Inchauspe, G.; Fujiawa, K.
 J. Gen. Virol. 73, 2725-2729, 1992
 A;Title: Genomic characterization and mutation rate of hepatitis C virus isolated from a
 A;Reference number: JQ1925; MUID: 93019030; PMID: 1383400
 A;Accession: JQ1926
 A;Molecule type: mRNA
 A;Residues: 1-523 <ABR>
 A;Cross-references: DBJ:010687
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: polyprotein
 C;Accession: C Product: C protein #status predicted <CPR>
 F;1191/Product: C protein #status predicted <CPR>
 F;1192-383/Product: E1 protein #status predicted <E1R>
 F;1194-523/Product: E2/NS1 protein #status predicted <E2P>
 Query Match 93.5%; Score 173; DB 2; Length 523;
 Best Local Similarity 88.2%; Pred. No. 1.7e-16; Mismatches 1; Indels 0; Gaps 0;
 Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: envelope protein

RESULT 30
 Query Match 93.0%; Score 172; DB 1; Length 3011;
 Best Local Similarity 91.2%; Pred. No. 1.7e-15; Mismatches 1; Indels 0; Gaps 0;
 Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 C;Accession: S19876
 R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
 submitted to the EMBL Data Library, September 1991
 A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
 A;Reference number: S18029
 A;Accession: S19876
 A;Molecule type: genomic RNA
 A;Residues: 1-782 <HON>

RESULT 31
 Query Match 93.0%; Score 172; DB 2; Length 782;
 Best Local Similarity 88.2%; Pred. No. 3.7e-16; Mismatches 3; Indels 1; Gaps 0; Gaps 0;
 Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 C;Species: hepatitis C virus
 C;Accession: A36814
 R;Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugianti, M.; Nasoff, M.; Prince, A.M.
 submitted to GenBank, July 1992
 A;Description: Genomic structure of the human prototype strain H of hepatitis C virus: c
 A;Reference number: A36814
 A;Molecule type: Genomic RNA
 A;Cross-references: UNIPROT:P27958; GB: M67463; NID: 932937; PID: AA45534.1; PIN: 9329738
 A;Cross-references: DBJ:010687
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: polyprotein
 C;Accession: C Product: C protein #status predicted <CPR>
 F;116-191/Product: envelope protein C #status predicted <CPC>
 F;122-389/Product: major envelope protein E #status predicted <EPM>
 F;130-729/Product: nonstructural protein NS1 #status predicted <MEB>
 F;330-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F;1007-1615/Product: hepacivin #status predicted <NS3>
 F;1230-1317/Region: nucleotide-binding motif B (P-loop)
 F;1312-1317/Region: nucleotide-binding motif B
 F;1316-1319/Region: DEXH motif
 F;1616-1862/Product: nonstructural protein NS4A #status predicted <NS4A>
 F;1863-2013/Product: nonstructural protein NS4B #status predicted <NS4B>
 F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
 F;1966, 209, 234, 305, 325, 417, 423, 430, 448, 476, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 2240, 23
 Query Match 93.0%; Score 172; DB 1; Length 3011;
 Best Local Similarity 91.2%; Pred. No. 1.7e-15; Mismatches 1; Indels 0; Gaps 0;
 Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 32
 Query Match 93.0%; Score 172; DB 1; Length 340;
 Best Local Similarity 88.2%; Pred. No. 3.7e-16; Mismatches 3; Indels 1; Gaps 0; Gaps 0;
 Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 C;Species: hepatitis C virus
 C;Accession: S19876
 R;Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugianti, M.; Nasoff, M.; Prince, A.M.
 submitted to GenBank, July 1992
 A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
 A;Reference number: S18029
 A;Accession: S19876
 A;Molecule type: genomic RNA
 A;Residues: 1-782 <HON>

C;Accession: S18031
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
Submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus isc
A;Reference number: S18029
A;Molecule type: genomic RNA
A;Residues: 1-782 <HOM>
A;Cross-references: UNIPROT:Q68950; EMBL:X61593

A;Experimental source: isolate JK2

C;Superfamily: hepatitis C virus genome polyprotein

C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural

F;1-91/Product: core protein #status predicted <MAT1>

F;192-383/Product: envelope protein 1 #status predicted <MAT2>

F;384-733/Product: NS1/E2 protein #status predicted <MAT3>

F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 91.9%; Score 170; DB 2; Length 782;

Best Local Similarity 88.2%; Pred. No. 7 2e-16; Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 307 SLYSGHVSGRVADMMNNWSPTTALVSQLRI 340

RESULT 33

JCS5620 genome polyprotein - hepatitis C virus (isolate EURL480)

N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructural protein NS4a); nonstructural protein NS4b; nonstructural protein NS5

C;Keywords: hepatitis C virus

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C;Accession: JCS5620

R;Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.

Biophys. Res. Commun. 236, 4449, 1997

A;Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant

A;Reference number: JCS5620; MUID:97366593; PMID:9223423

A;Molecule type: mRNA

A;Residues: 1-304 <CHA>

A;Cross-references: UNIPROT:O39928; GB:Y13184

A;Experimental source: genotype 5a, which predominates in South Africa

A;Note: the translation of the nucleotide sequence is not complete in this paper

C;Superfamily: hepatitis C virus genome polyprotein

C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin

F;2-15/Product: capsid protein C #status predicted <CP>

F;115-191/Product: envelope protein M #status predicted

F;192-389/Product: major envelope protein E #status predicted <ME>

F;384-408/Region: hypervariable #status predicted

F;730-730/Product: nonstructural protein NS1 #status predicted <NS1>

F;731-107/Product: nonstructural protein NS2 #status predicted <NS2>

F;1008-1616/Product: hepacivirin #status predicted <NS3>

F;1231-1238/Region: nucleotide-binding motif A (P-loop)

F;1313-1318/Region: nucleotide-binding motif B

F;1317-1320/Region: DEXH motif

F;1657-1833/Product: nonstructural protein NS4a #status predicted <NS4A>

F;1848-1849/Product: nonstructural protein NS4b #status predicted <NS4B>

F;2210-2249/Region: interferon sensitivity determining #status predicted

Query Match 87.6%; Score 162; DB 1; Length 3014;
Best Local Similarity 85.3%; Pred. No. 4.4e-14;
Matches 29; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Db 307 SLYSGHLSGRVADMMNNWSPAVGMVVAHVLRI 340

RESULT 36

PC2061 genome polyprotein N2 - hepatitis C virus

N;Contains: envelope protein E1; nonstructural protein B2/NS1

C;Species: hepatitis C virus

C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C;Accession: PC2061

R;Li, J.S.; Vitvitski, L.; Tong, S.P.; Trepo, C.

Biophys. Res. Commun. 199, 1474-1481, 1994

A;Title: Identification of the third major genotype of hepatitis C virus in France.

A;Reference number: PC2060; MUID:94197744; PMID:8147893

A;Molecule type: mRNA

A;Residues: 1-411 <LNU>

A;Cross-references: UNIPROT:Q81813; GB:LJ2355; MUID:9410169; PMID:AAA2015.1; PID:941170

C;Superfamily: hepatitis C virus genome polyprotein

C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6
Om protein - protein search, using sw model	
Run on:	November 10, 2004, 18:01:19 ; Search time 194 Seconds
Title:	US-10-685-435-15
Perfect score:	185
Sequence:	SIYPGHTITGHRMRAWDDMMNNNSPTTALVVSQRLI 34
Scoring table:	BLOSUM62
Searched:	Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters:	1825181
Minimum DB seq length: 0	
Maximum DB seq length: 200000000	
Post-processing:	Maximum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	UniProt_02: * 1: uniprot_sprot: * 2: uniprot_trembl: *
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No.	Score
1	185
2	185
3	185
4	185
5	185
6	185
7	185
8	185
9	185
10	185
11	185
12	185
13	185
14	185
15	185
16	185
17	185
18	184
19	184
20	184
21	184
22	184
23	184
24	184
25	184
26	184
27	184
28	184
29	184
30	184
31	184
Query	Match Length DB ID
	Description
1	185 100.0 119 2 Q80NH1
2	185 100.0 119 2 Q80NK9
3	185 100.0 119 2 Q80NLO
4	185 100.0 119 2 Q80NN4
5	185 100.0 154 2 Q91615
6	185 100.0 154 2 Q91616
7	185 100.0 154 2 Q91619
8	185 100.0 154 2 Q91650
9	185 100.0 154 2 Q91653
10	185 100.0 154 2 Q91654
11	185 100.0 154 2 Q91656
12	185 100.0 154 2 Q91657
13	185 100.0 154 2 Q91658
14	185 100.0 154 2 Q91659
15	185 100.0 154 2 Q8Q0E7
16	185 100.0 154 2 Q8Q0E8
17	185 100.0 3 1010
18	184 99.5 119 2 Q80NC7
19	184 99.5 119 2 Q80ND3
20	184 99.5 119 2 Q80NH2
21	184 99.5 119 2 Q80NH9
22	184 99.5 119 2 Q80NIO
23	184 99.5 119 2 Q80NIZ
24	184 99.5 119 2 Q80Nj4
25	184 99.5 119 2 Q80Nj5
26	184 99.5 119 2 Q80Nk4
27	184 99.5 119 2 Q80Nk5
28	184 99.5 119 2 Q80Nk6
29	184 99.5 119 2 Q80Nn9
30	184 99.5 119 2 Q80NNO
31	184 99.5 119 2 Q80NNI
32	184 99.5 119 2 Q80NN2
33	184 99.5 119 2 Q80NN3
34	184 99.5 154 2 Q916J1
35	184 99.5 154 2 Q916J2
36	184 99.5 154 2 Q916Q5
37	184 99.5 154 2 Q916Q9
38	184 99.5 154 2 Q916R0
39	184 99.5 154 2 Q916R1
40	184 99.5 154 2 Q916R2
41	184 99.5 154 2 Q916R3
42	184 99.5 154 2 Q916R6
43	184 99.5 154 2 Q916R7
44	184 99.5 154 2 Q916R8
45	184 99.5 154 2 Q916R9
ALIGNMENTS	
RESULT 1	
ID Q80NH1	PRELIMINARY;
ID Q80NH1	PRT; 119 AA.
AC Q80NH1;	Created)
DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)	
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)	
DE Envelope protein EI (Fragment).	
OS Hepatitis C virus.	
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;	
OC Hepacivirus.	
OX NCBI_TaxID=11103;	
[1]	
RESULT 2	
ID Q80NK9	PRELIMINARY;
ID Q80NK9;	PRT; 119 AA.
AC Q80NK9;	Created)
DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)	
DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)	
DE Envelope protein EI (Fragment).	
OS Hepatitis C virus.	
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;	
OC Hepacivirus.	
OX NCBI_TaxID=11103;	

RN [1] PRELIMINARY; PRT; 119 AA.
 RP ID 080NN4
 RX PRELIMINARY; PRT; 119 AA.
 MEDLINE=22447295; PubMed=12560577;
 RA AC 080NN4
 de Lambalierie J.-F., Biagini P., Attoui H., Gallian P., de Micco P.,
 "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients"; J. Gen. Virol. 84:441-446(2003).
 RL DR
 J. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF515874; AA083181.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR Pfam; PF01539; HCV env; I.
 DR Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON-TER 1 1
 FT NON-TER 119 119 MW; 96446DB861A8BC5AD CRC64;
 SQ SEQUENCE 119 AA; 13230 MW;
 Query Match 100.0%; Score 185; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Ov 1 SIYPGHTGHRMADMNMNSPTTALVWSQQLRI 34
 Db 78 SIYPGHTGHRMADMNMNSPTTALVWSQQLRI 111

RESULT 3
 080NLO PRELIMINARY; PRT; 119 AA.
 ID 080NLO
 AC 080NLO; PRELIMINARY; PRT; 119 AA.
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE Envelope protein E1 (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;

[1] PRELIMINARY; PRT; 119 AA.
 RN SEQUENCE FROM N.A.
 RP ID 080NLO
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 de Lambalierie X.,
 "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients"; J. Gen. Virol. 84:441-446(2003).
 RL DR
 J. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF515873; AA083180.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:019028; C:viral capsid; IEA.
 DR GO; GO:019011; C:viral envelope; IEA.
 DR InterPro; IPR002519; HCV env.
 DR Pfam; PF01539; HCV env; I.
 DR Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON-TER 1 1
 FT NON-TER 119 119 MW; 347247AD8E1568 CRC64;
 SQ SEQUENCE 119 AA; 13130 MW;
 Query Match 100.0%; Score 185; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 091615 PRELIMINARY; PRT; 154 AA.
 ID 091615
 AC 091615
 DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)
 DS Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;

[1] PRELIMINARY; PRT; 154 AA.
 RN SEQUENCE FROM N.A.
 RP ID 091615
 RX MEDLINE=2220166; PubMed=12404223;
 RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M.,
 Korber B., Perea A.S., Di Bisceglie A.M.;
 "Evolution of hepatitis C viral quasispecies after liver
 RT transplantation.",
 RL Gastroenterology 123:1485-1493(2002).
 DR EMBL; AF42264; AL124776.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR Pfam; PF01539; HCV env; I.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON-TER 1

RESULT 4

DR	GO; GO:0016021; C:integral to membrane; IEA.	DT	01-MAR-2004 (T-BEMBLrel. 26, last annotation update)
DR	GO; GO:0019028; C:viral capsid; IEA.	DE	Polyprotein.
DR	GO; GO:0019031; C:viral envelope; IEA.	OS	Repatitis C virus.
DR	GO; GO:0005198; F:structural molecule activity; IEA.	OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
DR	InterPro; IPR002519; HCV_env.	OC	Hepatitis C virus.
DR	InterPro; IPR002531; HCV_Ns1.	OX	Repatitis C virus.
DR	Pfam; PF01539; HCV_env; 1.	RN	SEQUENCE FROM N.A. [1]
DR	Pfam; PF01560; HCV_Ns1; 1.	RX	Medline=9335897; PubMed=8394876;
DR	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.	RA	Wang Y., Okamoto H., Tsuda F., Nagayama R., Tao Q.M., Mishiro S.;
FT	NON_TER 1	RT	"prevalence, genotypes, and an isolate (HC-C2) of hepatitis C virus in Chinese patients with liver disease.";
FT	154 154	RT	J. Med. Virol. 40:254-260(1993).
FT	154 AA; 16732 MW; 84EF18C0840C2122 CRC64;	RL	EMBL; D10934; BAA0128.1; -.
SQ	SEQUENCE 1 SIVPGHITGHRMAWDMMNNSPPTALVVSQRLI 34	DR	PIR; A61195; A61196.
QY	22 SIVPGHITGHRMAWDMMNNSPPTALVVSQRLI 55	DR	PIR; P00246; P00246.
Db	RESULT 16	DR	PIR; P00254; P00254.
Q8QEQ9	PRELIMINARY; PRT; 154 AA.	DR	PIR; P00804; P00804.
ID	0800E9	DR	PIR; P03029; P03029.
AC	Q8QEQ9; 01-JUN-2002 (T-BEMBLrel. 21, Created)	DR	HSSP; P2663; 1QUV.
DT	01-JUN-2002 (T-BEMBLrel. 21, Last sequence update)	DR	GO; GO:0016021; C:integral to membrane; IEA.
DT	01-JUN-2003 (T-BEMBLrel. 24, Last annotation update)	DR	GO; GO:0019028; C:viral capsid; IEA.
DE	E1/E2 Protein (Fragment).	DR	GO; GO:0003524; F:ATP binding; IEA.
OS	Hepatitis C virus.	DR	GO; GO:0003026; F:ATP-dependent helicase activity; IEA.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.	DR	GO; GO:0003723; F:RNA binding; IEA.
OC	Repatitis C virus.	DR	GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
OC	Ncbi_Taxid=1103; [1]	DR	GO; GO:0003236; F:serine-type peptidase activity; IEA.
RN	SEQUENCE FROM N.A.	DR	GO; GO:0005197; F:structural molecule activity; IEA.
RX	MEDLINE=22291660; PubMed=12404223;	DR	GO; GO:0005058; F:proteolysis and peptidolysis; IEA.
RA	Lyra A.C., Fan X., Lang D.M., Yusim K., Ramakhanlani S., Brunt E.M.,	DR	GO; GO:0003350; P:transcription; IEA.
RA	Korber B., Peralson A.S., Di Bisceglie A.M.; Evolution of hepatitis C viral quasispecies after liver transplantation.,"	DR	GO; GO:0019079; P:viral genome replication; IEA.
RT	Gastroenterology 123:1485-1493(2002).	DR	GO; GO:0019087; P:viral transformation; IEA.
RL	EMBL; AF497391; AAM19645.1;	DR	InterPro; IPR000345; CytC_heme_BS.
RL	DR; GO:0016021; C:integral to membrane; IEA.	DR	InterPro; IPR001410; DEAD.
DR	GO; 019028; C:viral capsid; IEA.	DR	InterPro; IPR00522; HCV_capsid.
DR	GO; 019031; C:viral envelope; IEA.	DR	InterPro; IPR00521; HCV_core.
DR	GO; 0005198; F:structural molecule activity; IEA.	DR	InterPro; IPR00519; HCV_env.
DR	InterPro; IPR002519; HCV_env.	DR	InterPro; IPR00531; HCV_Ns1.
DR	InterPro; IPR00531; HCV_Ns1.	DR	InterPro; IPR000745; HCV_Ns4a.
DR	DR; GO:0005198; F:structural molecule activity; IEA.	DR	InterPro; IPR001490; HCV_Ns4b.
DR	InterPro; IPR00861; HCV_Ns5a.	DR	InterPro; IPR00861; HCV_RdRp.
DR	InterPro; IPR00166; HCV_RdRp.	DR	InterPro; IPR001650; Helicase_C.
DR	InterPro; IPR004109; Peptidase_S29.	DR	InterPro; IPR004109; Peptidase_S29.
DR	InterPro; IPR009003; Pept_Ser_Tys.	DR	InterPro; IPR009003; Pept_Ser_Tys.
DR	InterPro; IPR002518; Pept_U39_HCV_Ns2.	DR	InterPro; IPR002518; Pept_U39_HCV_Ns2.
DR	InterPro; IPR000795; RNA_Pol_BS_PS.	DR	InterPro; IPR000795; RNA_Pol_BS_PS.
DR	InterPro; IPR007094; RNA_Pol_PsVir.	DR	InterPro; IPR007094; RNA_Pol_PsVir.
DR	Pfam; PF0143; HCV_capsid; 1.	DR	Pfam; PF0143; HCV_capsid; 1.
DR	Pfam; PF0142; HCV_core; 1.	DR	Pfam; PF0142; HCV_core; 1.
DR	Pfam; PF01539; HCV_env; 1.	DR	Pfam; PF01539; HCV_env; 1.
DR	Pfam; PF0160; HCV_Ns1; 1.	DR	Pfam; PF0160; HCV_Ns1; 1.
DR	Pfam; PF01538; HCV_Ns2; 1.	DR	Pfam; PF01538; HCV_Ns2; 1.
DR	Pfam; PF00907; HCV_Ns3; 1.	DR	Pfam; PF00907; HCV_Ns3; 1.
DR	Pfam; PF0106; HCV_Ns4a; 1.	DR	Pfam; PF0106; HCV_Ns4a; 1.
DR	Pfam; PF01001; HCV_Ns5a; 1.	DR	Pfam; PF01001; HCV_Ns5a; 1.
DR	Pfam; PF01506; HCV_Ns5a; 1.	DR	Pfam; PF01506; HCV_Ns5a; 1.
DR	Pfam; PF00211; HelicaseC; 1.	DR	Pfam; PF00211; HelicaseC; 1.
DR	Pfam; PF00938; Viral_RdRp; 1.	DR	Pfam; PF00938; Viral_RdRp; 1.
DR	SMART; SM00847; DEXDC; 1.	DR	SMART; SM00847; DEXDC; 1.
DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.	DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
DR	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.	DR	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
KW	SEQUENCE 3010 AA; 32687 MW; EATD306A4BA2B224 CRC64;	DR	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
QY	1 SIVPGHITGHRMAWDMMNNSPPTALVVSQRLI 34	DR	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
QY	22 SIVPGHITGHRMAWDMMNNSPPTALVVSQRLI 55	DR	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
RESULT 17	Query Match Best Local Similarity 100.0%; Score 185; DB 2; Length 154; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	Query Match Best Local Similarity 100.0%; Score 185; DB 2; Length 3010; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q1760	PRELIMINARY; PRT; 3010 AA.	DR	Query Match Best Local Similarity 100.0%; Score 185; DB 2; Length 3010; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID	081760	DR	Query Match Best Local Similarity 100.0%; Score 185; DB 2; Length 3010; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	081760;	DR	Query Match Best Local Similarity 100.0%; Score 185; DB 2; Length 3010; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	01-NOV-1996 (TREMBREL. 01, Created)	DR	Query Match Best Local Similarity 100.0%; Score 185; DB 2; Length 3010; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	01-NOV-1996 (TREMBREL. 01, Last sequence update)	DR	Query Match Best Local Similarity 100.0%; Score 185; DB 2; Length 3010; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18

ID Q8ONC7; PRELIMINARY; PRT; 119 AA.

AC Q8ONC7; PRELIMINARY; PRT; 119 AA.

DT 01-JUN-2003 (TREMBREL. 24, Created)

DT 01-JUN-2003 (TREMBREL. 24, Last sequence update)

DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DE Envelope protein E1 (Fragment).

OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

OC Hepacivirus.

OX NCBI_TaxID=1103;

RN [1]

RP SEQUENCE FROM N.A.

MDLINE=22447295; PubMed=12560577;

RX Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P., de Lamballerie X.; "Evolution of hepatitis C virus in blood donors and their respective recipients.", J. Gen. Virol. 84:441-446(2003).

RL EMBL; AF515956; AAC882631; -, Integral to membrane; IEA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:000518; F:structural molecule activity; IEA.

DR InterPro; IPR002519; HCV env.

DR Pfam; PF01539; HCV env; I.

KW Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON-TER 119 119

SEQUENCE 119 AA; 13164 MW; 7638FCF88D31EC1 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119; Best Local Similarity 97.1%; Pred. No. 1.5e-17; Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHTIGHRUAWDMMNNSPTALVVSQRLI 34

Db 78 SIYPGHTIGHRUAWDMMNNSPTALVVSQRLI 111

RESULT 19

ID Q8OND3; PRELIMINARY; PRT; 119 AA.

AC Q8OND3; PRELIMINARY; PRT; 119 AA.

DT 01-JUN-2003 (TREMBREL. 24, Created)

DT 01-JUN-2003 (TREMBREL. 24, Last sequence update)

DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DE Envelope protein E1 (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

OX NCBI_TaxID=1103;

RN [1]

RP SEQUENCE FROM N.A.

MDLINE=22447295; PubMed=12560577;

RX Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P., de Lamballerie X.; "Evolution of hepatitis C virus in blood donors and their respective recipients.", J. Gen. Virol. 84:441-446(2003).

RL EMBL; AF515911; AA0832181; -, Integral to membrane; IEA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR InterPro; IPR002519; HCV env.

DR Pfam; PF01539; HCV env; I.

KW Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON-TER 119 119

SEQUENCE 119 AA; 13091 MW; 789331FCB22E7F10 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119; Best Local Similarity 97.1%; Pred. No. 1.5e-17; Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHTIGHRUAWDMMNNSPTALVVSQRLI 34

Db 78 SIYPGHTIGHRUAWDMMNNSPTALVVSQRLI 111

RESULT 20

ID Q8ONH2; PRELIMINARY; PRT; 119 AA.

AC Q8ONH2; PRELIMINARY; PRT; 119 AA.

DT 01-JUN-2003 (TREMBREL. 24, Created)

DT 01-JUN-2003 (TREMBREL. 24, Last sequence update)

DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DE Envelope protein E1 (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

OX NCBI_TaxID=1103;

RN [1]

RP SEQUENCE FROM N.A.

MDLINE=22447295; PubMed=12560577;

RX Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P., de Lamballerie X.; "Evolution of hepatitis C virus in blood donors and their respective recipients.", J. Gen. Virol. 84:441-446(2003).

RL EMBL; AF515911; AA0832181; -, Integral to membrane; IEA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR InterPro; IPR002519; HCV env.

DR Pfam; PF01539; HCV env; I.

KW Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON-TER 119 119

SEQUENCE 119 AA; 13091 MW; 789331FCB22E7F10 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119; Best Local Similarity 97.1%; Pred. No. 1.5e-17; Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHTIGHRUAWDMMNNSPTALVVSQRLI 34

Db 78 SIYPGHTIGHRUAWDMMNNSPTALVVSQRLI 111

RESULT 21

ID Q8ONH9; PRELIMINARY; PRT; 119 AA.

AC Q8ONH9; PRELIMINARY; PRT; 119 AA.

DT 01-JUN-2003 (TREMBREL. 24, Created)

DT 01-JUN-2003 (TREMBREL. 24, Last sequence update)

DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DE Envelope protein E1 (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

OX NCBI_TaxID=1103;

RN [1]

RP SEQUENCE FROM N.A.

MDLINE=22447295; PubMed=12560577;

RX Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P., de Lamballerie X.; "Evolution of hepatitis C virus in blood donors and their respective recipients.", J. Gen. Virol. 84:441-446(2003).

RL EMBL; AF515950; AA0832571; -, Integral to membrane; IEA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR002519; HCV env.

DR Pfam; PF01539; HCV env; I.

KW Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON-TER 119 119

SEQUENCE 119 AA; 13252 MW; 6C593E1707341120 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119; Best Local Similarity 97.1%; Pred. No. 1.5e-17; Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHTIGHRUAWDMMNNSPTALVVSQRLI 34

Db 78 SIYPGHTIGHRUAWDMMNNSPTALVVSQRLI 111

RESULT 22

ID Q8ONH9; PRELIMINARY; PRT; 119 AA.

AC Q8ONH9; PRELIMINARY; PRT; 119 AA.

DT 01-JUN-2003 (TREMBREL. 24, Created)

DT 01-JUN-2003 (TREMBREL. 24, Last sequence update)

DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DE Envelope protein E1 (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

OX NCBI_TaxID=1103;

RN [1]

RP SEQUENCE FROM N.A.

MDLINE=22447295; PubMed=12560577;

RX Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P., de Lamballerie X.; "Evolution of hepatitis C virus in blood donors and their respective

RT recipients."; PRT; 119 AA.

RL J. Gen. Virol. 84:441-446(2003).

DR EMBL: AF515904; AA03211.1; "-; membrane; IEA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:005198; F:structural molecule activity; IEA.

DR InterPro; IPR002519; HCV env.

DR Pfam; PF01539; HCV env; 1.

KW Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON-TER 119 119

Qy 1 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 34

Db 78 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 111

RESULT 22

Q80N10 ID Q80N10 PRELIMINARY; PRT; 119 AA.

AC Q80N10; 01-JUN-2003 (TREMBrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DE Envelope protein E1 (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Replicivirus.

OX NCBI_TaxID=1103;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=2247295; PubMed=12560577;

RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P., de Lamballerie X.

RT "Evolution of hepatitis C virus in blood donors and their respective recipients"; J. Gen. Virol. 84:441-446(2003).

DR EMBL; AF515903; AA03210.1; "-.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:019028; C:viral capsid; IEA.

DR GO; GO:019031; C:viral envelope; IEA.

DR InterPro; IPR002519; HCV env.

DR Pfam; PF01539; HCV env; 1.

KW Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON-TER 119 119

Qy 1 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 34

Db 78 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 111

RESULT 22

Q80N10 ID Q80N10 PRELIMINARY; PRT; 119 AA.

AC Q80N10; 01-JUN-2003 (TREMBrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DE Envelope protein E1 (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Replicivirus.

OX NCBI_TaxID=1103;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=2247295; PubMed=12560577;

RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P., de Lamballerie X.

RT "Evolution of hepatitis C virus in blood donors and their respective recipients"; J. Gen. Virol. 84:441-446(2003).

DR EMBL; AF51889; AA08196.1; "-.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR InterPro; IPR002519; HCV env.

DR Pfam; PF01539; HCV env; 1.

KW Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON-TER 119 119

Qy 1 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 34

Db 78 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 111

RESULT 23

Q80N12 ID Q80N12 PRELIMINARY; PRT; 119 AA.

AC Q80N12; 01-JUN-2003 (TREMBrel. 24, Created)

DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)

Qy 1 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 34

Db 78 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 111

DE Envelope protein E1 (Fragment).

OS Hepatitis C virus. positive-strand viruses, no DNA stage; Flaviviridae; Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Replicivirus.

OX NCBI_TaxID=1103;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=2247295; PubMed=12560577;

RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P., de Lamballerie X.

RT "Evolution of hepatitis C virus in blood donors and their respective recipients"; J. Gen. Virol. 84:441-446(2003).

DR EMBL; AF51889; AA08196.1; "-.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR InterPro; IPR002519; HCV env.

DR Pfam; PF01539; HCV env; 1.

KW Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON-TER 119 119

Qy 1 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 34

Db 78 SIVPGHHTGHRMWAQDMMNNSPTTALVSQLRI 111

Db 78 SIVPGHVTGHRMADMNNWSPTALVSQLRI 111
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON-TER 1
 FT NON-TER 119 119
 FT NON-TER 119 AA; 13168 MW; 833357A8AB2D8A4 CRC64;
 SQ SEQUENCE
 RESULT 25
 ID Q8ONK5 PRELIMINARY; PRT; 119 AA.
 AC Q8ONK5;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Envelope protein EI (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=1103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RT "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.;"
 RL J. Gen. Virol. 84:441-446(2003).
 DR EMBL: AF515888; AAOB3195.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:000198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env. I.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 PT NON-TER 1 1
 FT NON-TER 119 119
 SQ SEQUENCE 119 AA; 13096 MW; 01FE4E9C16B0D3AC CRC64;
 Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17; 0; Indels 0; Gaps 0;
 Matches 33; Conservative 1; Mismatches 0;
 OX 1 SIVPGHVTGHRMADMNNWSPTALVSQLRI 34
 Db 78 SIVPGHVTGHRMADMNNWSPTALVSQLRI 111
 RESULT 26
 Q8ONK4 PRELIMINARY; PRT; 119 AA.
 AC Q8ONK4;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Envelope protein EI (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=1103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RT "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.;"
 RL J. Gen. Virol. 84:441-446(2003).
 DR EMBL: AF515879; AAOB3185.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env. I.
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 PT NON-TER 1 1
 FT NON-TER 119 119
 SQ SEQUENCE 119 AA; 13182 MW; 08B0BFP9328861ABA CRC64;
 Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17; 0; Indels 0; Gaps 0;
 Matches 33; Conservative 1; Mismatches 0;
 OX 1 SIVPGHVTGHRMADMNNWSPTALVSQLRI 34
 Db 78 SIVPGHVTGHRMADMNNWSPTALVSQLRI 111
 RESULT 28
 Q8ONK6 PRELIMINARY; PRT; 119 AA.
 AC Q8ONK6;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Envelope protein EI (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=1103;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=12560577;
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,

RA de Lamballerie X.; Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.; J. Gen. Virol. 84:441-446(2003).
 RL EMBL: AF515877; AA031841; -.
 DR GO; GO:016021; C:integral to membrane; IEA.
 DR GO; GO:019028; C:viral capsid; IEA.
 DR GO; GO:019031; C:viral envelope; IEA.
 DR GO; GO:005198; F:structural molecule activity; IEA.
 DR GO; PF002519; HCV env.
 DR Pfam; PF01539; HCV env; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 Transmembrane.

FT NON-TER 1 1
 FT NON-TER 119 119
 SQ SEQUENCE 119 AA; 13168 MW; 833357A3AB2DBAA4 CRC64;
 Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17; Mismatches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SIYPGHTGHRMADMNNWNSPTTALVVSQRLI 34
 Db 78 SIYPGHTGHRMADMNNWNSPTTALVVSQRLI 111

RESULT 29

080NM9 PRELIMINARY; PRT; 119 AA.
 ID 080NM9
 AC AA031601
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Envelope protein EL (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 NCBI_TaxID:11103;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447205; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RA de Lamballerie X.; Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.; J. Gen. Virol. 84:441-446(2003).
 RL EMBL; AF515854; AA031611; -.
 DR GO; GO:016021; C:integral to membrane; IEA.
 DR GO; GO:019028; C:viral capsid; IEA.
 DR GO; GO:019031; C:viral envelope; IEA.
 DR GO; GO:005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR Pfam; PF01539; HCV env; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 Transmembrane.

FT NON-TER 1 1
 SQ SEQUENCE 119 AA; 13168 MW; 833357A3AB2DBAA4 CRC64;
 Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17; Mismatches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SIYPGHTGHRMADMNNWNSPTTALVVSQRLI 34
 Db 78 SIYPGHTGHRMADMNNWNSPTTALVVSQRLI 111

RESULT 31

080NN1 PRELIMINARY; PRT; 119 AA.
 ID 080NN1
 AC AA031601
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Envelope protein EL (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 NCBI_TaxID:11103;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447205; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RA de Lamballerie X.; Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.; J. Gen. Virol. 84:441-446(2003).
 RL EMBL; AF51852; AA081159; 1
 DR GO; GO:016021; C:integral to membrane; IEA.
 DR GO; GO:019028; C:viral capsid; IEA.
 DR GO; GO:005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR Pfam; PF01539; HCV env; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 Transmembrane.

FT NON-TER 1 1
 SQ SEQUENCE 119 AA; 13146 MW; 5A0449DCD9A507C CRC64;
 Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17; Mismatches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 30

080NNO PRELIMINARY; PRT; 119 AA.
 ID 080NNO
 AC AA031601
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)

DR InterPro; IPR002519; HCV env.
 DR Pfam; PF01539; HCV env; I.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON-TER 1 1
 FT NON-TER 119 119
 SQ 119 AA; 13144 MW; 1F0EC961F9A8570C CRC64;

RESULT 32

Q80NN2 PRELIMINARY; PRT; 119 AA.

Q80NN2; 1 STYPGHTGHRMADMNMNSPTTALVSQLRI 34
 080NN2; 111

DR 01-JUN-2003 (T-EMBL; 24, Created)
 DT 01-JUN-2003 (T-EMBL; 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBL; 25, Last annotation update)

DE Envelope protein El (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TAXID=1103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=244795; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 de Lamballerie X.;
 RT "Evolution of hepatitis C virus in blood donors and their respective
 recipients.", J. Gen. Virol. 84:441-446(2003).
 RL J. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF51851; AAC03157.1; -;
 GO; GO:001621; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR InterPro; IPR002519; HCV env.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON-TER 1 1
 SQ SEQUENCE 119 AA; 13144 MW; 1F0EC961F9A8570C CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17; 0; Indels 0; Gaps 0;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Q80NN3 PRELIMINARY; PRT; 119 AA.

Q80NN3; 1 STYPGHTGHRMADMNMNSPTTALVSQLRI 34
 080NN3; 111

DR 01-JUN-2003 (T-EMBL; 24, Created)
 DT 01-JUN-2003 (T-EMBL; 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBL; 25, Last annotation update)

DE Envelope protein El (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TAXID=1103;

RESULT 33

Q80NN3 PRELIMINARY; PRT; 119 AA.

Q80NN3; 1 STYPGHTGHRMADMNMNSPTTALVSQLRI 34
 080NN3; 111

DR 01-JUN-2003 (T-EMBL; 24, Created)
 DT 01-JUN-2003 (T-EMBL; 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBL; 25, Last annotation update)

DE Envelope protein El (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TAXID=1103;

RP SEQUENCE FROM N.A.
 RX MEDLINE=244795; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 de Lamballerie X.;
 RT "Evolution of hepatitis C virus in blood donors and their respective
 recipients.", J. Gen. Virol. 84:441-446(2003).
 RL J. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF51851; AAC03157.1; -;
 GO; GO:001621; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR InterPro; IPR002519; HCV NS1.
 DR Pfam; PF01539; HCV env; I.
 DR PPN150; HCV NS1; I.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON-TER 1 1
 SQ SEQUENCE 154 AA; 1668 MW; 6DDE98C02F8F9907 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 154;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17; 0; Indels 0; Gaps 0;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Q80NN4 PRELIMINARY; PRT; 154 AA.

Q80NN4; 1 STYPGHTGHRMADMNMNSPTTALVSQLRI 34
 080NN4; 55

DR 01-JUN-2003 (T-EMBL; 24, Created)
 DT 01-JUN-2003 (T-EMBL; 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBL; 25, Last annotation update)

DE Envelope protein El (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TAXID=1103;

RESULT 35

Q916J2 PRELIMINARY; PRT; 154 AA.

Q916J2; 1
 AC 0916J2;
 DT 01-DEC-2001 (T-EMBL; 19, Created)
 DT 01-DEC-2001 (T-EMBL; 19, Last sequence update)
 DT 01-JUN-2003 (T-EMBL; 24, Last annotation update)

DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.

OX	NCBI_TAXID=11103;	QY	1 SIVPGHGTGHRMADMDDMNNSPTTALVSQLRI 34
RN	[1] SSEQUENCE FROM N.A. PubMed=12404223;	Db	22 SIVPGHGTGHRMADMDDMNNSPTTALVSQLRI 55
RX	MEDLINE=22291660; PubMed=12404223;		
RA	Lyra, A.C., Pan, X., Lang, D.M., Yusim, K., Ramrakhiani, S., Brunt, E.M.,		
RA	Korber, B., Persson, A.S., Di Bisceglie, A.M.;		
RT	"Evolution of hepatitis C viral quasispecies after liver		
RT	Gastroenterology 123:1485-1493 (2002).		
RL	Gastroenterology 123:1485-1493 (2002).		
DR	EMBL: AF422457; AAL24769_1; -		
DR	GO: 0016021; C:integral to membrane; IEA.		
DR	GO; GO:0019028; C:viral capsid; IEA.		
DR	GO; GO:0019031; C:viral envelope; IEA.		
DR	GO; GO:00198; R:structural molecule activity; IEA.		
DR	InterPro; IPR002519; HCV env.		
DR	InterPro; IPR002531; HCV NS1.		
DR	PF01539; HCV env; I.		
DR	PF01560; HCV NS1; I.		
KW	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;		
KW	Polyprotein; Transmembrane.		
FT	NON TER <1 >154 AA; 15718 MW;		
FT	CHAIN 1 <1 >154 envelope glycoprotein E1/E2.		
FT	NON TER 154 AA; 15718 MW;		
FT	SEQUENCE 154 AA; 16718 MW;		
QY	Query Match 99.5%; Score 184; DB 2; length 154;		
Matches	Best Local Similarity 97.1%; Pred. No. 1.9e-17; 1; Mismatches 0; Indels 0; Gaps 0;		
Db	1 SIVPGHGTGHRMADMDDMNNSPTTALVSQLRI 34		
Db	22 SIVPGHGTGHRMADMDDMNNSPTTALVSQLRI 55		
RESULT 36			
Q916Q5	PRELIMINARY; PRT; 154 AA.		
ID	Q916Q5; PRELIMINARY; PRT; 154 AA.		
AC	Q916Q5; PRELIMINARY; PRT; 154 AA.		
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)		
DT	01-JUN-2003 (TREMBrel. 24, Last annotation update)		
DE	Polyprotein (Fragment).		
OS	Hepatitis C virus.		
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;		
OC	Reoviridae.		
OX	NCBI_TaxID=1103;		
RN	[1] SSEQUENCE FROM N.A. PubMed=12404223;		
RX	MEDLINE=22291660; PubMed=12404223;		
RA	Lyra, A.C., Pan, X., Lang, D.M., Yusim, K., Ramrakhiani, S., Brunt, E.M.,		
RA	Korber, B., Persson, A.S., Di Bisceglie, A.M.;		
RT	"Evolution of hepatitis C viral quasispecies after liver		
RT	Gastroenterology 123:1485-1493 (2002).		
RL	Gastroenterology 123:1485-1493 (2002).		
DR	EMBL: AF422394; AAL24706_1; -		
DR	GO; GO: 0016021; C:integral to membrane; IEA.		
DR	GO; 01928; C:viral capsid; IEA.		
DR	GO; GO:019031; C:viral envelope; IEA.		
DR	GO; GO:000539; R:structural molecule activity; IEA.		
DR	InterPro; IPR002519; HCV env.		
DR	PF01539; HCV env; I.		
DR	PF01560; HCV NS1; I.		
KW	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;		
KW	Polyprotein; Transmembrane.		
FT	NON TER <1 >154 AA; 16723 MW;		
FT	CHAIN 1 <1 >154 envelope glycoprotein E1/E2.		
FT	NON TER 154 AA; 16723 MW;		
FT	SEQUENCE 154 AA; 16723 MW;		
QY	Query Match 99.5%; Score 184; DB 2; length 154;		
Matches	Best Local Similarity 97.1%; Pred. No. 1.9e-17; 1; Mismatches 0; Indels 0; Gaps 0;		
Db	1 SIVPGHGTGHRMADMDDMNNSPTTALVSQLRI 34		
Db	22 SIVPGHGTGHRMADMDDMNNSPTTALVSQLRI 55		
RESULT 38			
Q916R0	PRELIMINARY; PRT; 154 AA.		
ID	Q916R0; PRELIMINARY; PRT; 154 AA.		
AC	Q916R0; PRELIMINARY; PRT; 154 AA.		
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)		
DT	01-JUN-2003 (TREMBrel. 24, Last annotation update)		
DE	Polyprotein (Fragment).		
OS	Hepatitis C virus.		
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;		
OC	Reoviridae.		
OX	NCBI_TaxID=1103;		
RN	[1] SSEQUENCE FROM N.A. PubMed=12404223;		
RX	MEDLINE=22291660; PubMed=12404223;		
RA	Lyra, A.C., Pan, X., Lang, D.M., Yusim, K., Ramrakhiani, S., Brunt, E.M.,		
RA	Korber, B., Persson, A.S., Di Bisceglie, A.M.;		
RT	"Evolution of hepatitis C viral quasispecies after liver		
RT	Gastroenterology 123:1485-1493 (2002).		
RL	Gastroenterology 123:1485-1493 (2002).		
DR	EMBL: AF422389; AAL24701_1; -		
DR	GO; GO: 0016021; C:integral to membrane; IEA.		

DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA. activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR InterPro; IPR02531; HCV NS1.
 DR Pfam; PF01539; HCV env; 1.
 DR Coat protein; Env⁺ope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON-TER <1 1 envelope glycoprotein E1/E2.
 FT CHAIN <1 >154 154 envelope glycoprotein E1/E2.
 FT NON-TER 154 154 envelope glycoprotein E1/E2.
 SQ SEQUENCE 154 AA; 16737 MW; 9E56EB988D5C189F CRC64;

Query Match 99.5%; Score 184; DB 2; Length 154;
 Best Local Similarity 97.1%; Pred. No. 1.9e-17; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SIYPGHTGHRMADMNMNSPTTALVVSQQLRI 34
 22 SIYPGHTGHRMADMNMNSPTTALVVSQQLRI 55

RESULT 39

Q916R1 PRELIMINARY; PRT; 154 AA.
 ID Q916R1 PRELIMINARY; PRT; 154 AA.
 AC Q916R1; 1
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Herpesvirus; OC NCBITaxonID=1103;

RP SEQUENCE FROM N.A.

RN [1]

RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramzakhiani S., Brunt E.M.,
 RA Korber B., Peralta A.S., Di Bisceglie A.M.;
 RA "Evolution of hepatitis C viral quasispecies after liver
 transplantation";
 RL Gastroenterology 123:1405-1433 (2002).
 DR InterPro; IPR002531; HCV env.
 DR Pfam; PF01539; HCV env; 1.
 DR Coat protein; Env⁺ope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON-TER <1 1 envelope glycoprotein E1/E2.
 FT CHAIN <1 >154 154 envelope glycoprotein E1/E2.
 FT NON-TER 154 154 envelope glycoprotein E1/E2.
 SQ SEQUENCE 154 AA; 16771 MW; 70B2A5D9CDF61895 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 154;
 Best Local Similarity 97.1%; Pred. No. 1.9e-17; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SIYPGHTGHRMADMNMNSPTTALVVSQQLRI 34
 22 SIYPGHTGHRMADMNMNSPTTALVVSQQLRI 55

Search completed: November 10, 2004, 18:17:54
 Job time: 195 secs

RESULT 40

Q916R2 PRELIMINARY; PRT; 154 AA.
 ID Q916R2 PRELIMINARY; PRT; 154 AA.
 AC 0916R2; IPR02531; HCV env.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)

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